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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 70 Seconds
(without alignments)
243.107 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192
Sequence: 1 ANAFLLXLRPGSLRXKCKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	44	2	AAU18305 Human fac
2	172	89.6	44	4	AAB36395 Human fac
3	172	89.6	44	7	ADD50096 Human vit
4	172	89.6	44	8	ADQ26902 Human fac
5	172	89.6	401	4	AAB84870 Mutant bl
6	172	89.6	401	4	AAB84871 Mutant bl
7	172	89.6	406	2	AAR35764 Factor VI
8	172	89.6	406	2	AAW14510 Modified
9	172	89.6	406	2	AAW14509 Modified
10	172	89.6	406	4	AAU77745 Human fac
11	172	89.6	406	4	AAB84867 Mutant bl
12	172	89.6	406	4	AAB84868 Mutant bl
13	172	89.6	406	4	AAB84869 Mutant bl
14	172	89.6	406	4	AAB84866 Wild-type
15	172	89.6	406	4	AAW52183 Human FVI
16	172	89.6	406	4	AAW52172 Mammalian
17	172	89.6	406	4	AAW52186 Human FVI
18	172	89.6	406	4	AAW52171 Human FVI
19	172	89.6	406	4	AAW52187 Human FVI
20	172	89.6	406	4	AAW52181 Human FVI
21	172	89.6	406	4	AAW52185 Human FVI
22	172	89.6	406	4	AAW52184 Human FVI
23	172	89.6	406	4	AAW52182 Human FVI
24	172	89.6	406	5	AAU77196 Human coa
25	172	89.6	406	5	AAU77191 Human coa

26	172	89.6	406	5	AAU77200 Human coa
27	172	89.6	406	5	AAU77192 Human coa
28	172	89.6	406	5	AAU77190 Human coa
29	172	89.6	406	5	AAU77198 Human coa
30	172	89.6	406	5	AAU77193 Human coa
31	172	89.6	406	5	AAU77199 Human coa
32	172	89.6	406	5	AAU79201 Human coa
33	172	89.6	406	5	AAU77188 Human coa
34	172	89.6	406	5	AAU77194 Human coa
35	172	89.6	406	5	AAU77195 Human coa
36	172	89.6	406	5	AAU77189 Human coa
37	172	89.6	406	5	AAU77197 Human coa
38	172	89.6	406	5	ABG31688 Human coa
39	172	89.6	406	5	ABB09178 Human fac
40	172	89.6	406	5	ABB80051 Human coa
41	172	89.6	406	5	ABB80069 Human coa
42	172	89.6	406	5	ABB80072 Human coa
43	172	89.6	406	5	ABB80071 Human coa
44	172	89.6	406	5	ABB80068 Human coa
45	172	89.6	406	5	ABB80070 Human coa

ALIGNMENTS

RESULT 1
AAU18305
ID AAU18305 standard; peptide; 44 AA.
XX
AC AAU18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX
FN WO9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US022152.
XX
PR 23-OCT-1997; 97US-00955636.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
XX
SQ Sequence 44 AA;

KW aspirin; warfarin; heparin; haemophilic disorder; haemostatic;
 KW anticoagulant; factor VII.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1. .44
 FT /label= OTHER
 FT /note= "OTHER= All Xaa residues are glutamic acid or
 FT gamma carboxyglutamic acid"
 FT
 XX
 XX
 PN US6747003-B1.
 XX
 XX
 PD 08-JUN-2004.
 XX
 XX
 PF 03-FEB-2000; 2000US-00497591.
 XX
 XX 23-OCT-1997; 97US-00955636.
 PR 29-APR-1999; 99US-00302239.
 XX
 XX (MINU) UNIV MINNESOTA.
 PA
 XX
 XX Nelsestuen GL;
 PI
 XX
 XX WPI; 2004-429803/40.
 DR
 XX
 XX
 PT Decreasing clot formation by administering an anticoagulant agent, and a
 PT protein C or activated protein C polypeptide having a modified GLA
 PT domain, useful for treating hemophilic disorders in mammals.
 PT
 XX
 PS Example 5; SEQ ID NO 3; 4lpp; English.
 XX
 XX The invention relates to a method of decreasing clot formation comprising
 CC administering to a patient an anticoagulant agent and a protein C or
 CC activated protein C (APC) polypeptide comprising a modified gamma-
 CC carboxyglutamic acid (GLA) domain with two, three, four or five amino
 CC acid substitutions. The invention also relates to vitamin K-dependent
 CC nucleic acids, polypeptides, host cells, vectors and antibodies used in
 CC the methods of the invention. The anticoagulant agent is aspirin,
 CC warfarin or heparin, preferably aspirin. The methods and compositions of
 CC the present invention are useful for modulating clot formation for
 CC treating haemophilic disorders in mammals. This sequence represents the
 CC human factor VII GLA domain, used in the method of the invention.
 XX
 SQ Sequence 44 AA;
 Query Match 89.6%; Score 172; DB 8; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.2e-21; Mismatches 0; Indels 0; Gaps 0;
 Matches 44; Conservative 0;
 QY 1 ANAFLLXLRPGSLRXKCKXQCSPFXRXRIFKDAKRTKLFWISY 44
 DB 1 ANAFLLXLRPGSLRXKCKXQCSPFXRXRIFKDAKRTKLFWISY 44
 RESULT 5
 AAB84870
 ID AAB84870 standard; protein; 401 AA.
 XX
 AC AAB84870;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-31).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

FT
 FT
 XX
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-00237610.
 XX
 PR 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX
 PS Claim 14; Page 20-21; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 401 AA;
 Query Match 89.6%; Score 172; DB 4; Length 401;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRPGSLRXKCKXQCSPFXRXRIFKDAKRTKLFWISY 44
 DB 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 6
 AAB84871
 ID AAB84871 standard; protein; 401 AA.
 XX
 AC AAB84871;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 235. .239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 PF 24-AUG-1999; 99JP-00237610.
 XX
 PR 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.

FT	Modified-site	35	/note= "proteolytic site"
FT			/label= OTHER
FT	Cleavage-site	38. .39	/note= "gamma-carboxyglutamic acid"
FT			/note= "proteolytic site"
FT	Cleavage-site	42. .43	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Cleavage-site	44. .45	/note= "proteolytic site"
FT			/note= "proteolytic site"
FT	Disulfide-bond	50. .61	
FT	Disulfide-bond	55. .70	
FT	Modified-site	63	
FT			/label= OTHER
FT			/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72. .81	
FT	Disulfide-bond	91. .102	
FT	Disulfide-bond	98. .112	
FT	Disulfide-bond	114. .127	
FT	Disulfide-bond	135. .162	
FT	Cleavage-site	143. .144	
FT			/note= "proteolytic site"
FT	Modified-site	145	
FT			/note= "glycosylation site"
FT	Disulfide-bond	159. .164	
FT	Disulfide-bond	178. .194	
FT	Active-site	193	
FT	Active-site	242	
FT	Cleavage-site	290. .291	
FT			/note= "proteolytic site"
FT	Disulfide-bond	310. .329	
FT	Cleavage-site	315. .316	
FT			/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference	315	
FT			/note= "native Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"
FT			
FT	Modified-site	322	
FT			/note= "glycosylation site"
FT	Disulfide-bond	340. .368	
FT	Cleavage-site	341. .342	
FT			/note= "proteolytic site"
FT	Active-site	344	
FT	Cleavage-site	392. .393	
FT			/note= "proteolytic site"
FT	Cleavage-site	396. .397	
FT			/note= "proteolytic site"
FT	Cleavage-site	402. .403	
FT			/note= "proteolytic site"
XX			
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	22-AUG-1994;	94US-00293778.	
XX			
PR	13-NOV-1989;	89US-00434149.	
PR	12-JUN-1992;	92US-00898248.	
PR	09-AUG-1993;	93US-00104509.	
XX			
XX	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;		
XX			
DR	WPI; 1997-033523/03.		
XX			
XX	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability.		
PT			
XX			
PS	Example 4; Page; 28pp; English.		
XX			
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Ile42, Tyr44, Phe378, Arg290, Arg304, Tyr332 and Lys341 by an		

CC	amino acid that provides a proteolytically more stable peptide bond.									
CC	provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.									
CC	The modified proteins are useful for treating bleeding disorders such as									
CC	thrombocytopenia and von Willebrand's disease. They are also suitable for									
CC	addition to plasma substitutes. The present sequence is a specific									
CC	example of a modified factor VII protein.. (Updated on 25-MAR-2003 to									
CC	correct PF field.)									
XX										
SQ	Sequence 406 AA;									
	Query Match	89.6%	Score 172;	DB 2;	Length 406;					
	Best Local Similarity	77.3%	Pred. No. 1.2e-20;							
	Matches 34;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;					
Qy	1	ANAFLLXLRPGSLRXKXKXCSFXXARXIFKDAARTKLFWISY	44							
Db	1	ANAFLELRPGSLRECKEQCSPFEAREIFKDAERTKLFWISY	44							
RESULT 9										
AAW14509										
ID	AAW14509 standard; protein; 406 AA.									
XX										
AC	AAW14509;									
XX										
XX	25-MAR-2003 (revised)									
DT	14-MAY-1997 (first entry)									
XX										
DE	Modified blood coagulation Factor VII (R290S).									
XX										
KW	Blood coagulation; factor 7; mutant; mutation; modification;									
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.									
XX										
OS	Homo sapiens.									
OS	Synthetic.									
XX										
PH	Key	Location/Qualifiers								
FT	Modified-site	6								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	7								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	14								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	16								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Disulfide-bond	17. .22								
FT	Modified-site	19								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	20								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	25								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	26								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	29								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	32. .33								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Modified-site	35								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Cleavage-site	38. .39								
FT		/label= OTHER								
FT		/note= "proteolytic site"								
FT	Modified-site	42. .43								
FT		/label= OTHER								
FT		/note= "gamma-carboxyglutamic acid"								
FT	Cleavage-site	42. .43								
FT		/label= OTHER								
FT		/note= "proteolytic site"								

FT Cleavage-site /note= "proteolytic site"
FT 44. .45
FT /note= "proteolytic site"
FT 50. .61
FT Disulfide-bond
FT Disulfide-bond 55. .70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT 72. .81
FT Disulfide-bond 91. .102
FT Disulfide-bond 98. .112
FT Disulfide-bond 114. .127
FT Disulfide-bond 135. .162
FT Cleavage-site 143. .144
FT /note= "proteolytic site"
FT 145
FT /note= "glycosylation site"
FT 159. .164
FT Disulfide-bond 178. .194
FT Active-site 193
FT Active-site 242
FT Cleavage-site 290. .291
FT /note= "proteolytic site in unmodified factor VII"
FT 290
FT /note= "native Arg290 has been substituted by Ser to
FT provide a proteolytically more stable peptide bond"
FT 310. .329
FT Cleavage-site 315. .316
FT /note= "proteolytic site"
FT 322
FT /note= "glycosylation site"
FT 340. .368
FT Cleavage-site 341. .342
FT /note= "proteolytic site"
FT 344
FT Active-site 392. .393
FT Cleavage-site 396. .397
FT /note= "proteolytic site"
FT 402. .403
FT /note= "proteolytic site"
FT
FT
PN US5580560-A.
XX
XX 03-DEC-1996.
XX
XX 22-AUG-1994; 94US-00293778.
XX
XX 13-NOV-1989; 89US-00434149.
XX 12-JUN-1992; 92US-00898248.
XX 09-AUG-1993; 93US-00104509.
XX
XX (NOVO) NOVO-NORDISK AS.
XX
XX Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid substitutions
XX to improve proteolytic stability.
XX
XX Example 3; Page; 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32, Lys38,
XX Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an
XX amino acid that provides a proteolytically more stable peptide bond,
XX provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
XX The modified proteins are useful for treating bleeding disorders such as
XX thrombocytopenia and von Willebrand's disease. They are also suitable for
XX addition to plasma substitutes. The present sequence is a specific
XX example of a modified factor VII protein. (Updated on 25-MAR-2003 to
XX correct PF field.)
XX

XX SQ Sequence 406 AA;
XX
XX Query Match 89.6%; Score 172; DB 2; Length 406;
XX Best Local Similarity 77.3%; Pred. No. 1.2e-20;
XX Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
XX
XX QY 1 ANAFLLXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44
XX
XX RESULT 10
XX AAU77745
XX ID AAU77745 standard; protein; 406 AA.
XX
XX AC AAU77745;
XX
XX DT 05-JUN-2002 (first entry)
XX
XX DE Human factor VIIa active site mutant.
XX
XX KW Factor VIIa; human; shock heat treatment; protein stability;
XX KW protein manufacture; protein conformation; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Active-site 193
FT /note= "Member of the factor VIIa catalytic triad"
FT Active-site 242
FT /note= "Member of the factor VIIa catalytic triad"
FT Misc-difference 344
FT /label= Gly, Met, Thr
FT /note= "Preferably Ala. Wild type Ser"
FT Active-site 344
FT /note= "Member of the factor VIIa catalytic triad"
XX
XX WQ20017141-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-DK000234.
XX
XX 06-APR-2000; 2000DK-00000573.
XX 17-APR-2000; 2000US-0197850P.
XX
XX (NOVO) NOVO NORDISK AS.
XX
XX Matthiesen F;
XX
XX WPI; 2001-657162/75.
XX
XX Stabilization of a polypeptide e.g. in a pharmaceutical composition
XX involves a shock heat treatment.
XX
XX Disclosure; Page; 22pp; English.
XX
XX The invention describes a method of stabilising a polypeptide involving
XX shock heat treatment of the polypeptide. The method is useful in a
XX pharmaceutical composition, in the industrial or large scale method of
XX manufacturing a polypeptide, also as a unit operation during preparation,
XX purification, recovery and/or formulation of polypeptides. The shock heat
XX treatment improves the protein stability without substantial loss of
XX biological activity. The method can be applied to change polypeptide
XX conformation in a very fast and non-invasive manner. The polypeptide
XX formed is stable. The method is also useful for decreasing the
XX association of the polypeptide. This sequence represents a modified human
XX factor VIIa protein, mutated at the catalytic site, described in the
XX invention. Note: This sequence does not appear in the specification but
XX has been obtained using information given in the invention
XX

```
SQ      Sequence 406 AA;

Query Match      89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLXRXCKXXQCSPFXKXARXIFKDAKRTKLFWISY 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 44

RESULT 11
AAB84867
ID      AAB84867 standard; protein; 406 AA.
XX
AC      AAB84867;
XX
DT      31-JUL-2001 (first entry)
XX
DE      Mutant blood coagulant factor VII (FVII-5).
XX
KW      Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW      mutant; mutain.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 159
FT      /note= "Wild-type Cys substituted by Ala"
FT      Misc-difference 164
FT      /note= "Wild-type Cys substituted by Ala"
FT      Misc-difference 164
FT      /note= "Wild-type Cys substituted by Ala"
XX
PN      JP2001061479-A.
XX
PD      13-MAR-2001.
XX
PF      24-AUG-1999; 99JP-00237610.
XX
PR      24-AUG-1999; 99JP-00237610.
XX
PA      (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR      WPI; 2001-310677/33.
DR      N-PSDB; AAH19460.
XX
PT      Mutant of blood coagulant factor VII, used for substitution therapy in
PT      the treatment of hemophilia.
XX
PS      Claim 3; Page 11-12; 29pp; Japanese.
XX
CC      The present invention relates to mutants of blood coagulant factor VII
CC      (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC      sequence is one such mutant FVII: VII-5. In the wild-type protein
CC      (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
CC      protein, the disulphide bond is disrupted. The mutants can be used as an
CC      agent for the substitution therapy of haemophilia inhibitor patients
XX
SQ      Sequence 406 AA;

Query Match      89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.2e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      1 ANAFLLXLRPGSLXRXCKXXQCSPFXKXARXIFKDAKRTKLFWISY 44
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 ANAFLELRPGSLRECKEQQCFEAREIFKDAERTKLFWISY 44

RESULT 12
AAB84868
ID      AAB84868 standard; protein; 406 AA.
XX
```

FT XX Arg-Lys-Thr-Leu"
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 PF
 XX 24-AUG-1999; 99JP-00237610.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2001-310677/33.
 DR
 DR N-PSDB; AAH19462.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX Claim 9; Page 17-18; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 CC
 XX Sequence 406 AA;
 SQ
 Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRPGSLRXKXQCXQCSFXXARXIFKDAERTKLFWISY 44
 DB 1 ANAFLEELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 14
 ID AAB84866
 AA AAB84866 standard; protein; 406 AA.
 AC AAB84866;
 XX
 XX 31-JUL-2001 (first entry)
 DT
 XX Wild-type human blood coagulant factor VII (FVII).
 DE
 XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 6 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 7 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 14 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19 /label= Glu, OTHER
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 FT
 FT Misc-difference 20 /label= Glu, OTHER
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 FT
 FT Misc-difference 25 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
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 FT Misc-difference 26 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52 /note= "O-glycosylated"
 FT
 FT Modified-site 60 /note= "O-glycosylated"
 FT
 FT Modified-site 145 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 FT /notes= "proteolytic cleavage site converting FVII zymogen
 CC to an activated form, comprising two chains linked by a

CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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 DB 1 ANAFLEELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 44
 FT
 RESULT 15
 ID AAM52183
 AA AAM52183 standard; protein; 406 AA.
 AC AAM52183;
 XX
 XX 07-FEB-2002 (first entry)
 DT
 XX Human FVII mutant V253N.
 DE
 XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutein.
 OS
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH
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 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 7 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
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 FT Misc-difference 14 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 20 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 25 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 26 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35 /label= Glu, OTHER
 FT /notes= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52 /note= "O-glycosylated"
 FT
 FT Modified-site 60 /note= "O-glycosylated"
 FT
 FT Modified-site 145 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153
 FT /notes= "proteolytic cleavage site converting FVII zymogen
 CC to an activated form, comprising two chains linked by a

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 15 Seconds
(without alignments)
282.236 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFXXLRPGSLRXCKXX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	466	1 KFHU7	coagulation factor
2	138	71.9	443	2 I46932	coagulation factor
3	123	64.1	407	1 KFB07	coagulation factor
4	109	56.8	461	1 JX0210	protein C (activat
5	104	54.2	456	1 KXBO	coagulation factor
6	102	53.1	488	1 EXHU	coagulation factor
7	101	52.6	492	1 EXBO	protein C (activat
8	100	52.1	461	1 S18994	coagulation factor
9	96	50.0	482	1 EXRT	coagulation factor
10	91	47.4	475	1 EXCH	coagulation factor
11	86	44.8	416	1 KFB0	protein C (activat
12	84	43.8	461	1 KXHU	coagulation factor
13	83	43.2	461	1 T8HU	thrombin (EC 3.4.2
14	83	43.2	622	1 KFHU	thrombin (EC 3.4.2
15	79	41.1	617	2 S10511	thrombin (EC 3.4.2
16	79	41.1	618	2 A35827	coagulation factor
17	78	40.6	452	1 A30351	coagulation factor
18	78	40.6	459	2 JQ0419	probable MAP kinase
19	71.5	37.2	576	2 G96763	probable MAP kinase
20	69	35.9	642	2 S53433	plasma protein S p
21	66	34.4	675	1 KXBOS	plasma protein S p
22	65.5	34.1	594	2 D84859	probable MAP kinase
23	65.5	34.1	603	2 C96575	probable MAP kinase
24	64	33.3	642	2 S53434	plasma protein S p
25	64	33.3	646	2 S38819	plasma protein S p
26	64	33.3	676	1 KXHUS	plasma protein Z p
27	63	32.8	396	1 KXBOZ	thrombin (EC 3.4.2
28	63	32.8	625	1 TBBO	thrombin (EC 3.4.2
29	63	32.8	675	1 KXRTS	plasma protein S p

RESULT 1

KFHU7

Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C:Accession: A28322; A23819; A31186; B31186; S63524

R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murra

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende

A:Reference number: A28322; MUID:87260948; PMID:3037537

A:Accession: A28322

A:Molecule type: DNA

A:Residues: 1-466 <OHA>

A:Cross-references: UNIPROT:P08709; GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334

R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A:Title: Characterization of a cDNA coding for human factor VII.

A:Reference number: A23819; MUID:86205965; PMID:3486420

A:Accession: A23819

A:Molecule type: mRNA

A:Residues: 1-466 <HAG>

A:Cross-references: GB:M13232; NID:g182799; PIDN:AAA8040.1; PID:g182801

R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F

Biochemistry 27, 7785-7793, 1988

A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a fi

A:Reference number: A90539; MUID:89088153; PMID:3264725

A:Accession: A31186

A:Molecule type: protein

A:Residues: 61-212 <THI>

A:Accession: B31186

A:Molecule type: protein

A:Residues: 213-466 <TH2>

R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A:Reference number: A40529; MUID:91250411; PMID:1904059

A:Contents: annotation; carbohydrate binding sites

R:Persson, E.; Petersen, L.C.

Eur. J. Biochem. 234, 233-300, 1995

A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A:Reference number: S63524; MUID:96096752; PMID:8529655

A:Accession: S63524

A:Molecule type: protein

C:Genetics:

A:Gene: GDB:F7

A:Cross-references: GDB:119897; OMIM:227500

A:Map position: 13q34-13q34

A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser
coagulation factor IX in the presence of calcium and tissue factor

F;30-39/Domain: propeptide #status predicted <PRO>
F;40-194/Product: protein C light chain #status experimental <LCH>
F;98-128/Domain: EGF homology <EG1>
F;137-172/Domain: EGF homology <EG2>
F;197-456/Product: protein C heavy chain #status experimental <HCH>
F;211-440/Domain: activation peptide #status experimental <APT>
F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;119-128,137-148,144-157,159-172,180-318,323,368-382,393-421/Disulfide bonds: #statu
F;136,289,350/Binding site: carbohydrate (Aasn) (covalent) #status predicted
F;236,298,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carbohydrate (Aasn) (covalent) #status predicted

Query Match 54.2%; Score 104; DB 1; Length 456;
Best Local Similarity 45.5%; Pred. No. 1.3e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFELXLRPGSLRXCKKXCQSFXXARXIFKDAYRTKLFWISY 44
||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 40 ANSFLLELPQNVERECSEVCEPEAREIFQNTDTMAFWFSFY 83
||:|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N;Alternate names: Stuart factor
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 09-Jul-2004
C;Accession: A24478; JQ0917; A2485; A25853; A22208; A21284; A20362; S39415; I54051; A050
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e
A;Reference number: A24478; MUID:87026600; PMID:3768336
A;Accession: A24478
A;Molecule type: DNA
A;Residues: 1-488 <LEV>
A;Cross-references: UNIPROT:P00742; GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; I
R;Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
A;Reference number: JQ0917; MUID:91216473; PMID:1902434
A;Accession: JQ0917
A;Molecule type: mRNA
A;Residues: 1-488 <MES>
A;Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
E;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
A;Reference number: A42485; MUID:92218390; PMID:1313796
A;Accession: A42485
A;Molecule type: DNA
A;Residues: 1-15 <MIA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
A;Accession: A25853
A;Molecule type: mRNA
A;Residues: 19-284, 'E', 289-488 <KAU>
A;Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336
E;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA coding for human blood coagulat
A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Accession: A22208
A;Molecule type: mRNA
A;Residues: 13-441, 'S', 443-488 <FUN>
A;Cross-references: GB:X03194; NID:g182840; PIDN:AAA52490.1; PID:g182841
R;Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:84222026; PMID:6587384
A;Accession: A21284
A;Molecule type: mRNA
A;Residues: 13-284, 'E', 289-488 <LE2>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation factor X
A;Reference number: A20362; MUID:83257207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
A;Residues: 41-179 <MCM>
R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39415
A;Molecule type: protein
A;Residues: 183-234 <INO>
A;Note: glycosylation sites
A;Note: Identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G. Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X
A;Reference number: I54051; MUID:90128299; PMID:2612918
A;Accession: I54051
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M33297; NID:G183860; PIDN:AAAS2636.1; PID:G553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A;Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-cysteine
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor X
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: GDB:119890; OMIM:227600
A;Map position: 13q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EGI>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-234/Domain: activation peptide #status experimental <APT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;57-62/Disulfide bonds: #status predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;103/Modified site: carboxylate (Thr) (covalent) #status experimental
F;199,211/Binding site: carboxylate (Thr) (covalent) #status experimental
F;221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
F;234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 53.18; Score 102; DB 1; Length 488;
Best Local Similarity 40.98; Pred. No. 2.9e-09;
Matches 16; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
1 ANAFXXLRPGLXRCXCKXQCSFXARXIFKDXRKLFWISY 44

Db 41 ANSFLEEMKKGHLRECMETCSYEAREVFEDSKTNEPMKY 84
RESULT 7
EXBO
coagulation factor Xa (BC 3.4.21.6) precursor - bovine
N;Alternate names: Stuart factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
A;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A. Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a signal peptide
A;Reference number: A22867; MUID:84247315; PMID:6330671
A;Accession: A22867
A;Molecule type: mRNA
A;Residues: 1-487 <FUN>
A;Cross-references: UNIPROT:P00743; GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K. Biochemistry 19, 659-667, 1980
A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A;Reference number: A14997; MUID:80130563; PMID:6766735
A;Accession: A14997
A;Molecule type: protein
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Contents: annotation; revision to residue 103
R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H. Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A;Reference number: A12030; MUID:76053069; PMID:1059093
A;Accession: A12030
A;Molecule type: protein
A;Residues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <TJ>
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, I.; Oehlin, A.K.; Stenflo, J. J. Biol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal factor X
A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
A;Molecule type: protein
A;Residues: 85-126 <PER>
A;Note: beta-hydroxyaspartic acid site
R;Inoue, K.; Morita, T. Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39414
A;Molecule type: protein
A;Residues: 183-196;199-209;216-233 <INO>
A;Note: carboxylate binding sites
R;Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; Davies, E.W. Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian factor X
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davies, E.W. Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to factor Xb
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J. J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid
A;Reference number: A38024; MUID:84185716; PMID:6546930
R;Morita, T.; Jackson, C.M. J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800

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Query Match      52.1%; Score 100; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 6.1e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
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Gene 169, 269-273, 1996

A;Experimental Source: COS-1 Cell
R;Enyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plac
A;Reference number: PS0190; MUID:92041742; PMID:1718949
A;Accession: PS0191
A;Molecule type: protein
A;Residues: 41-58, 'X', 60-65 <ENJ1>
A;Accession: PS0190
A;Molecule type: protein
A;Residues: 183-186, 'X', 188-207 <ENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of t
A;Reference number: 146196; MUID:94222160; PMID:8168596
A;Accession: I62745
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 295-383, 'G', 385-455 <MUR>
A;Cross-references: GB:D21215; NID:G415309; PIDN:BA04756.1; PID:G455396
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pro
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EG1>

F;110/Binding site: carbohydrate (Thr) (covalent) #status absent
F;113/Modified site: erythro-beta-hydroxypartate acid (Asp) #status experimental
F;139_290_355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;211-212/Cleavage site: Arg-Leu (Chromin) #status experimental
F;253_299_402/Active site: His, Asp, Ser #status predicted
F;371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 43.8%; Score 84; DB 1; Length 461;
Best Local Similarity 43.9%; Pred. No. 3.1e-06;
Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAPLXXLRPGSLXKXCXOCSPFXAXRXPFKDAXRTKLFW 41
||:||||| |||| | :||:: ||
DB 43 ANSFLERHSSLRECIIEICDFEAKEIFONVDOTLAPW 83

RESULT 13

KFHU

N;Alternate names: antihaemophilic factor B; Christmas factor
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A20302
R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A;Reference number: A00922; UID:86000558; PMID:2994716
A;Accession: A00922
A;Molecule type: DNA
A;Residues: 1-461 <YOS>
A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; PIDN:AAB59620.1; PID:g182613
R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Brown
EMBO J, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; UID:84236100; PMID:6329734
A;Accession: A37570
A;Molecule type: DNA
A;Residues: 1-461 <ANS>
A;Cross-references: GB:K02048
R;Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemsma, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
A;Reference number: A30511; UID:88327116; PMID:3416069
A;Accession: A30511
A;Molecule type: DNA
A;Residues: 8-24 <REI>
A;Cross-references: EMBL:X55008; NID:G311288; PIDN:CAB38245.2; PID:G4469253
R;Koerberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am J Hum Genet. 45, 448-457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymor
A;Reference number: A32989; UID:89371752; PMID:2773937
A;Accession: A32989
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 10-92 <YOS>
R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A;Reference number: A22673; UID:85190593; PMID:3857619
A;Accession: A22673
A;Molecule type: mRNA
A;Residues: 1-193,'T',195-461 <MCG>
A;Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A;Note: the authors translated the codon ACA for residue 29 as Tyr
R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstoshe
Nucleic Acids Res. 11, 2325-2335, 1983
A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-bas
A;Reference number: A21337; UID:83220788; PMID:6687940
A;Accession: A21337
A;Molecule type: mRNA
A;Residues: 1-193,'T',195-461 <JAY>
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611

R; Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T. Somat. Cell Mol. Genet. 10, 465-473, 1984

A; Title: Isolation and characterization of human factor IX cDNA: identification of Tag I

A; Reference number: A37546; MUID:84300526; PMID:6089357

A; Accession: A37546

A; Molecule type: mRNA

A; Residues: 38-193, 'T', 195-326 <JAG>

A; Cross-references: GB:M35672

R; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982

A; Title: Isolation and characterization of a cDNA coding for human factor IX.

A; Reference number: A30623; MUID:83065193; PMID:6959130

A; Accession: A30623

A; Molecule type: mRNA

A; Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',

A; Cross-references: GB:J00136; NID:9182608; PIDN:AA98726.1; PID:9182609

A; Experimental source: liver

R; Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.

Vox Sang. 58, 21-29, 1990

A; Title: Development of an immunoaffinity process for factor IX purification.

A; Reference number: A60486; MUID:90194857; PMID:2316207

A; Accession: A60486

A; Molecule type: protein

A; Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>

R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A; Reference number: A20274; MUID:83308813; PMID:6688526

A; Accession: A20274

A; Molecule type: protein

A; Residues: 105-109, 'X', 111-115 <MCM>

R; Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle

Eur. J. Biochem. 172, 565-572, 1988

A; Title: Characterisation of two differently processed forms of human recombinant factor

A; Reference number: S02527; MUID:88166735; PMID:3280312

A; Accession: S02527

A; Molecule type: protein

A; Residues: 29-63 <BAL>

A; Note: processed forms expressed in recombinant system

R; Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,

EMBO J. 9, 3295-3301, 1990

A; Title: Characterization of recombinant human Factor IX expressed in transgenic mice an

A; Reference number: S12058; MUID:91006024; PMID:2209546

A; Accession: S12058

A; Molecule type: mRNA; protein

A; Residues: 1-68 <JAL>

A; Note: processed forms expressed in recombinant system

R; Hanford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe

EMBO J. 9, 475-480, 1990

A; Title: The first EGF-like domain from human factor IX contains a high-affinity calcium

A; Reference number: S12377; MUID:90151623; PMID:2406129

A; Accession: S12377

A; Molecule type: protein

A; Residues: 92-130 <HAN>

A; Note: NMR detection of calcium binding by domain expressed in recombinant system

R; de la Salle, C.; Charnantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,

Thromb. Haemost. 70, 370-371, 1993

A; Title: A deletion located in the 3' non translated part of the factor IX gene responsi

A; Reference number: S159612; MUID:94054330; PMID:8236150

A; Accession: S159612

A; Status: translated

A; Status: translated from GB/EMBL/DBDJ

A; Molecule type: DNA

A; Residues: 444-461 <RES>

A; Cross-references: GB:S66752; NID:9439773; PIDN:AAB28588.1; PID:9439774

R; Scofield, E.S.; Koerber, D.D.; Sarkar, G.; Sommer, S.S.

Science 239, 491-494, 1988

A; Title: Genomic amplification with transcript sequencing.

A; Reference number: S159529; MUID:88127096; PMID:3340835

A; Accession: S159529

A; Status: translated from GB/EMBL/DBDJ

A; Molecule type: DNA

A; Residues: 290-359 <RE2>

A; Cross-references: GB:M19063; NID:9182622; PIDN:AAA52456.1; PID:9182623

R; Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iwe

Biochemistry 33, 5167-5171, 1994

A; Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin

A; Reference number: A54255; MUID:94227047; PMID:8172892

A; Accession: A54255

A; Molecule type: protein

A; Residues: 'D', 204, 'X', 206-211, 'D', 214, 'X', 216-221, 'D' <AGA>

A; Note: the residues designated 'X' were determined to be threonine bound to carbohydrate

R; Di Scipio, R.G.; Kurachi, K.; Davie, E.W.

J. Clin. Invest. 61, 1528-1538, 1978

A; Title: Activation of human factor IX (Christmas factor).

A; Reference number: A18483; MUID:78194509; PMID:659613

A; Contents: annotation; activation; active site; carbohydrate binding

R; McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.

Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984

A; Reference number: A37569

A; Contents: annotation

A; Note: 194-Thr was also found

R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 259, 5698-5704, 1984

A; Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding

A; Reference number: A37543; MUID:84185715; PMID:6425296

A; Contents: annotation; calcium binding

R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.

J. Biol. Chem. 260, 2583, 1985

A; Reference number: A37544

A; Contents: annotation; calcium binding, correction

R; Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.

Cell 45, 343-348, 1986

A; Title: Defective propeptide processing of blood clotting factor IX caused by mutation c

A; Reference number: A37545; MUID:86189947; PMID:3009023

A; Contents: annotation; signal sequence cleavage site

R; Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,

J. Biol. Chem. 264, 21257-21265, 1989

A; Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan

A; Reference number: A30622; MUID:90078229; PMID:2592373

A; Contents: annotation; sequence of mutant B(M) Nagoya

R; Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee

submitted to the Brookhaven Protein Data Bank, November 1991

A; Reference number: A51252; PID:IXA

A; Contents: annotation; conformation by (1)H-NMR, residues 92-130

A; Note: recombinant form expressed in yeast

C; Comment: Factor IX is activated by factor Xla, which excises the activation peptide pro

C; Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-

C; Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro

C; Genetics:

A; Gene: GDB:F9

A; Cross-references: GDB:119900; OMIM:306900

A; Map position: Xq27.1-Xq27.2

A; Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1

C; Function:

A; Description: catalyzes the proteolytic activation of coagulation factor X in the preser

A; Pathway: blood coagulation intrinsic pathway

C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F; 1-28/Domain: signal sequence #status predicted <SIG>

F; 29-46/Domain: propeptide #status experimental <PPT>

F; 31-91/Domain: Gla domain homology <GLA>

F; 47-191/Product: coagulation factor IXa light chain #status experimental <ALC>

F; 97-128/Domain: EGF homology <EG1>

F; 134-170/Domain: EGF homology <EG2>

F; 192-226/Domain: activation peptide #status experimental <ACT>

F; 227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>

F; 227-454/Domain: trypsin homology <TRY>

F; 53, 54, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #st

F; 64-69, 97-108, 102-117, 119-128, 134-145, 141-155, 157-170, 178-335, 252-268, 382-396, 407-435/Df

F; 99/Binding site: carbohydrate (ser) (covalent) #status experimental

F; 110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F; 191-192/Cleavage site: Arg-Ala (coagulation factor Xla) #status experimental

F; 203, 213/Binding site: carbohydrate (Asn) (covalent) #status experimental

F; 205, 217/Binding site: carbohydrate (Thr) (covalent) #status experimental

F; 226-227/Cleavage site: Arg-Val (coagulation factor Xla) #status experimental

Query Match 43.2%; Score 83; DB 1; Length 461;
Best Local Similarity 44.1%; Pred. No. 4.6e-06;
Matches 15; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 11 GSLXRCXKXQCSFFXARXFKDAXRTKLFWISY 44
DB 58 GNLERECMEKCSFEAREVTFENTERTTFWKQY 91

RESULT 14
TBHU
thrombin (EC 3.4.21.5) precursor [validated] - human
N:Alternate names: coagulation factor II
N:Contents: prothrombin
C:Species: Homo sapiens (man)
C:Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A29351; A00914; B00914; A37549; A37550; I51952
R:Degen, S.J.F.; Davie, E.W., 1987
Biochemistry 26, 6165-6177, 1987
A:Title: Nucleotide sequence of the gene for human prothrombin.
A:Reference number: A29351; MUID:88077877; PMID:2825773
A:Accession: A29351
A:Molecule type: DNA
A:Residues: 1-822 <DE>
A:Cross-references: UNIPROT:P00734; GB:M17262; GB:M33691; NID:G558069; PIDN:AAC63054.1;
R:Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.,
Biochemistry 22, 2087-2097, 1983
A:Title: Characterization of the complementary deoxyribonucleic acid and gene coding for
A:Reference number: A00914; MUID:83231469; PMID:6305407
A:Accession: A00914
A:Molecule type: mRNA
A:Residues: 8-163, 'N', 165-622 <DE2>
A:Cross-references: GB:V00595; GB:J00307; PIDN:CAA23842.1; PID:G1335344
A:Accession: B00914
A:Molecule type: DNA
A:Residues: 188-311 <DE3>
R:Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.,
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
J. Biol. Chem. 252, 4942-4957, 1977
A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
A:Reference number: A37549; MUID:77193964; PMID:266717
A:Accession: A37549
A:Molecule type: protein
A:Residues: 44-118, 'N', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-308,
R:Butkowsk, R.J.; Ellison, J.; Downing, M.R.; Mann, K.G.,
J. Biol. Chem. 252, 4942-4957, 1977
A:Title: Primary structure of human prothrombin 2 and alpha-thrombin.
A:Reference number: A37550; MUID:77207112; PMID:873923
A:Accession: A37550
A:Molecule type: protein
A:Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
R:Rabiet, M.J.; Blashill, A.; Furie, B.; Furie, B.C.,
J. Biol. Chem. 261, 13210-13215, 1986
A:Reference number: A37551; MUID:87008532; PMID:3759958
A:Contents: annotation; activation cleavages
R:MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.,
Ann. N.Y. Acad. Sci. 485, 73-78, 1986
A:Title: Recombinant genetic approaches to functional mapping of thrombin.
A:Reference number: I51952; MUID:87182874; PMID:3471151
A:Accession: I51952
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2, 'R', 5-100 <RES>
A:Cross-references: GB:M33031; NID:G190723; PIDN:AAA60220.1; PID:G190724
C:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin
C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds
C:Comment: can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain
ter 314-Arg, are released in natural blood clotting.
C:Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C:Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy
ent interaction with the negatively charged phospholipid membrane surface.
C:Comment: The prothrombin precursor is synthesized in the liver.
C:Genetics:
A:Gene: GDB:12

A:Cross-references: GDB:119894; OMIM:176930
A:Map position: lip11-11q12
A:Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/2
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: acute phase; blood coagulation; kringle homology; calcium binding; carboxyglutamic acid; duplicate
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-87/Domain: Gla domain homology <GLA>
F:44-622/Product: prothrombin #status experimental <MAT>
F:108-186/Domain: activation peptide #status experimental <APT>
F:108-186/Domain: kringle homology <KR1>
F:213-291/Domain: kringle homology <KR2>
F:328-363/Product: thrombin light chain #status experimental <LCH>
F:364-622/Product: thrombin heavy chain #status experimental <HC>
F:364-613/Domain: trypsin homology <TRY>
F:49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
F:121,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:336-482,536-550,564-594/Disulfide bonds: #status predicted
F:391-407/Disulfide bonds: #status experimental
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carboxylate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental

Query Match 43.2%; Score 83; DB 1; Length 622;
Best Local Similarity 36.4%; Pred. No. 6e-06;
Matches 16; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

OY 1 ANAPFLXLRPGSLXRXCKXQCSFFXARXFKDAXRTKLFWISY 44
DB 44 ANTFLEVRKGNLERECVEETCSVEEAPALESTATDVFWKY 87

RESULT 15
S10511
thrombin (EC 3.4.21.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C:Accession: S10511; A60576; B42696
R:Dihanich, M.; Monard, D.,
Nucleic Acids Res. 18, 4251, 1990
A:Title: cDNA sequence of rat prothrombin.
A:Reference number: S10511; MUID:90332426; PMID:2377469
A:Accession: S10511
A:Molecule type: mRNA
A:Residues: 1-617 <DIH>
A:Cross-references: UNIPROT:P18292; EMBL:X52835; NID:G56969; PIDN:CAA37017.1; PID:G56970
R:Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.,
Endocrinology 126, 167-175, 1990
A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A:Reference number: A60576; MUID:90091942; PMID:2293980
A:Accession: A60576
A:Molecule type: protein
A:Residues: 44-58 <HEN>
A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uter
R:Banfield, D.K.; MacGillivray, R.T.A.,
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequ
A:Reference number: A42696; MUID:92212913; PMID:1557383
A:Accession: B42696
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 383-617, 'E' <BAN>
A:Cross-references: GB:M81397
C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C:Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-43/Domain: propeptide #status predicted <PRO>
F:28-88/Domain: Gla domain homology <GLA>
F:44-617/Product: prothrombin #status experimental <PMAT>
F:109-187/Domain: kringle homology <KR1>
F:215-292/Domain: kringle homology <KR2>
F:360-609/Domain: trypsin homology <TRY>

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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 174 Seconds
(without alignments)
129.491 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFLLXLRPGSLRXKCKX.....XXARXIFKDAIXRTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	172	89.6	466	1	FA7_HUMAN
2	172	89.6	679	2	Q96FQ8
3	138	71.9	444	1	FA7_RABIT
4	127	66.1	446	1	FA7_MOUSE
5	123	64.1	407	1	FA7_BOVIN
6	114	59.4	459	1	PRTC_PIG
7	109	56.8	460	1	PRTC_MOUSE
8	104	54.2	446	1	FA7_RAT
9	104	54.2	456	1	PRTC_BOVIN
10	102	53.1	443	2	Q8JHC9
11	102	53.1	488	1	FA10_HUMAN
12	101	52.6	425	2	Q8Q4X7
13	101	52.6	492	1	FA10_BOVIN
14	100	52.1	461	1	PRTC_RAT
15	100	52.1	461	2	Q68FY8
16	99	51.6	218	1	TMG1_HUMAN
17	99	51.6	266	2	Q8NEK6
18	99	51.6	433	2	Q8Q4X5
19	98	51.0	490	1	FA10_RABIT
20	96	50.0	482	1	FA10_RAT
21	95	49.5	434	2	Q7T3B6
22	94	49.0	340	2	Q8QY26
23	94	49.0	458	1	PRTC_RABIT
24	94	49.0	469	2	Q9GMD9
25	94	49.0	481	1	FA10_MOUSE
26	93	48.4	456	1	PRTC_CANFA
27	92	47.9	228	2	Q6IP17
28	92	47.9	229	2	Q8J340
29	92	47.9	251	2	Q6DDE6
30	92	47.9	376	1	FA10_TROCA
31	92	47.9	432	2	Q6GNA2

32	91	47.4	475	1	FA10_CHICK	P25155 gallus gall
33	90	46.9	376	1	FA10_HOFSF	P83370 holocephal
34	90	46.9	524	2	Q7SXH8	Q7exh8 brachydanio
35	89	46.4	179	2	Q8TAS3	Q8tas3 homo sapien
36	89	46.4	198	1	TMG2_MOUSE	Q8r182 mus musculus
37	89	46.4	202	1	TMG2_HUMAN	O14669 homo sapien
38	89	46.4	537	2	Q8Q4X8	Q8Q4w8 fugu rubrip
39	88	45.8	231	1	TMG3_HUMAN	Q9bzd7 homo sapien
40	88	45.8	231	2	Q8N2N6	Q8n2n6 homo sapien
41	88	45.8	250	2	Q6PAQ9	Q6paq9 mus musculus
42	88	45.8	462	2	Q6PAG2	Q6pag2 xenopus lae
43	87.5	45.6	208	2	Q6GPL7	O6gpl7 xenopus lae
44	87.5	45.6	216	2	Q6DIH4	O6dih4 xenopus tro
45	87	45.3	442	2	Q8Q4X1	Q8Q4x1 fugu rubrip

ALIGNMENTS

RESULT 1
FA7_HUMAN
ID - FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (SPCA) (Proconvertin) (Eptacog alfa).
GN Name=F7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.B., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Inley M.Y., Kisiel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Inley M.Y.,
RA Hagen F.S., Murrat M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
[3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
[5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RP MEDLINE=91250411; PubMed=1904059;
RX Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kisiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine.";

RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-
RT Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor VIIa
RT with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANT GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patrachini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Caonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7).";
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94284305; PubMed=8204879;
RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT SER-367.
RX PubMed=7860081;
RA Dewald G., Noeche M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of
RT human complement component C7.";
RL Hum. Hered. 44:301-304(1994).
RN [17]
RP VARIANT VAL-354.
RX MEDLINE=95072599; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [18]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [19]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [20]
RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU2>3.3.CO;2-6;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [21]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
RA Seligsohn U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RL Thromb. Haemost. 76:283-291(1996).
RN [22]
RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
RT the signal sequence identified in a patient with factor VII
RT deficiency.";
RL Br. J. Haematol. 101:47-49(1998).
RN [23]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene.";

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RL Hum. Mutat. Suppl. 1:S189-S191(1998).
RN [24]

Query Match      89.6%; Score 172; DB 1; Length 466;
Best Local Similarity 77.3%; Pred. No. 4.3e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFXLXLRPGSLRXKCKXXCQSPFXARXIFPKDAXRTKLFWISY 44
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Db 61 ANAFLELRPGSLRECKEQCSFEAREIFPKDAERTKLFWISY 104

RESULT 2
ID Q96PQ8 PRELIMINARY; PRT; 679 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX "NCBI_TaxID=9606;
   [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
   cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -.
DR HSSP; P08709; IKLI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA_1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;
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Query Match      89.6%; Score 172; DB 2; Length 679;
Best Local Similarity 77.3%; Pred. No. 6.4e-22;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFXLXLRPGSLRXKCKXXCQSPFXARXIFPKDAXRTKLFWISY 44
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFPKDAERTKLFWISY 82

RESULT 3
ID FA7_RABIT STANDARD; PRT; 444 AA.
AC P98I39; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
   conversion accelerator).
GN Name=PF7;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
   [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
   factor VII.";
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RL TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Initiates the extrinsic pathway of blood coagulation.
   Serine protease that circulates in the blood in a zymogen form.
   Factor VII is converted to factor VIIa by factor Xa, factor XIIa,
   factor IXa, or thrombin by minor proteolysis. In the presence of
   tissue factor and calcium ions, factor VIIa then converts factor X
   to factor Xa by limited proteolysis. Factor VIIa will also convert
   factor IX to factor IXa in the presence of tissue factor and
   calcium (By similarity).
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
   form factor Xa.
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
   a disulfide bond (By similarity).
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
   glutamate residues allows the modified protein to bind calcium (By
   similarity).
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
   domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation -
   the European Bioinformatics Institute. There are no restrictions on its
   use by non-profit institutions as long as its content is in no way
   modified and this statement is not removed. Usage by and for commercial
   entities requires a license agreement (See http://www.ebi.ac.uk/ebis/
   or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U77477; AAB37326.1; -.
CC HSSP; P08709; 1FAK.
CC MEROPS; S01.215; -.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
DR
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InterPro; IPR006209; EGF like.
 InterPro; IPR002383; GLA_blood.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR009003; Pept_ser_Cys.
 InterPro; IPR000294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; GLA; 1.
 Pfam; PF00089; Trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00010; EGFBLD.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00069; EGF_CA; 1.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLA_1; 1.
 PROSITE; PS00098; GLA_2; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Blood coagulation; Calcium-binding; EGF-like domain;
 Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
 SIGNAL 1 21 Potential.
 FT PROPEP 22 39 Potential.
 FT CHAIN 40 191 Factor VII light chain.
 FT CHAIN 192 444 Factor VII heavy chain.
 FT DOMAIN 40 84 GLA.
 FT DOMAIN 85 121 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 126 167 EGF-like 2.
 FT DOMAIN 192 444 Serine protease.
 FT SITE 191 192 Cleavage (by factor Xa, factor XIa, factor IXa, or thrombin) (By similarity).
 FT ACT_SITE 232 232 By similarity.
 FT ACT_SITE 281 281 By similarity.
 FT ACT_SITE 383 383 By similarity.
 FT BINDING 377 377 Substrate (By similarity).
 FT DISULFID 56 61 By similarity.
 FT DISULFID 89 100 By similarity.
 FT DISULFID 94 109 By similarity.
 FT DISULFID 111 120 By similarity.
 FT DISULFID 130 141 By similarity.
 FT DISULFID 137 151 By similarity.
 FT DISULFID 153 166 By similarity.
 FT DISULFID 174 301 By similarity.
 FT DISULFID 198 203 By similarity.
 FT DISULFID 217 233 By similarity.
 FT DISULFID 349 368 By similarity.
 FT DISULFID 379 407 By similarity.
 FT MOD_RES 45 45 4-carboxyglutamate.
 FT MOD_RES 46 46 4-carboxyglutamate.
 FT MOD_RES 53 53 4-carboxyglutamate.
 FT MOD_RES 55 55 4-carboxyglutamate.
 FT MOD_RES 58 58 4-carboxyglutamate.
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 FT MOD_RES 64 64 4-carboxyglutamate.
 FT MOD_RES 65 65 4-carboxyglutamate.
 FT MOD_RES 68 68 4-carboxyglutamate.
 FT MOD_RES 74 74 4-carboxyglutamate.
 FT MOD_RES 102 102 3-hydroxyaspartate (By similarity).
 FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 242 242 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
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Query Match 71.9%; Score 138; DB 1; Length 444;
 Best Local Similarity 59.1%; Pred. No. 5.6e-16;
 Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXXQCSFXAXRIFKDXRTKLFWSY 44
 DB 40 ANSFLELRPGSLRECKBELCSFEAREVFQSTERTKQFWITY 83
 RESULT 4
 ID FA7 MOUSE STANDARD; PRT; 446 AA.
 AC P70375; Q61109;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 DE Names: P7; Synonyms: Ccf7;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D., Castellino F.J.;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D., Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487 (1996).
 [2]
 RP SEQUENCE FROM N.A.
 RN MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine blood coagulation factor VII gene.";
 RL Thromb. Haemost. 76:957-964 (1996).
 CC -!- FUNCTION: Initiates the extrinsic pathway of blood coagulation. Serine protease that circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIa, factor IXa or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor Xa by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium (By similarity).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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 EMBL; U44795; AAC52570.1; -;
 EMBL; U66079; AAC33796.1; -;
 HSSP; P08709; 1BF9.
 MEROPS; S01.215; -;
 MGD; MGI:109325; F7.
 InterPro; IPR000152; Asx_hydroxyl_S.
 InterPro; IPR000742; EGF_2.
 InterPro; IPR001881; EGF_Ca.
 InterPro; IPR001438; EGF_II.


```

DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
KW Repeat; Serine protease; Signal; Vitamin K.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 41 By similarity.
FT CHAIN 42 459 Vitamin K-dependent protein C.
FT CHAIN 42 196 Vitamin K-dependent protein C light chain
FT CHAIN 199 459 (By similarity).
FT CHAIN 199 459 (By similarity).
FT PEPTIDE 199 213 Activation peptide (By similarity).
FT SITE 213 214 Cleavage (by thrombin) (By similarity).
FT DOMAIN 42 87 EGF-like 1.
FT DOMAIN 96 131 EGF-like 2.
FT DOMAIN 135 175 Serine protease.
FT DOMAIN 214 459
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
FT ACT_SITE 225 225 Charge relay system.
FT ACT_SITE 301 301 Charge relay system.
FT ACT_SITE 400 400 Charge relay system.
FT DISULFID 58 63 By similarity.
FT DISULFID 91 110 By similarity.
FT DISULFID 100 105 By similarity.
FT DISULFID 104 119 By similarity.
FT DISULFID 121 130 By similarity.
FT DISULFID 139 150 By similarity.
FT DISULFID 146 159 By similarity.
FT DISULFID 161 174 By similarity.
FT DISULFID 182 321 Interchain (By similarity).
FT DISULFID 240 256 By similarity.
FT DISULFID 371 385 By similarity.
FT DISULFID 396 424 By similarity.
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 59.4%; Score 114; DB 1; Length 459;
Best Local Similarity 50.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKCKXQCSFXRXARXIFKDXRXTKLFWSY 44
DB 42 ANSFLLELRPSSLRCKEETCDFEAREIFONTWAFWSKY 85

RESULT 7
PRTC_MOUSE
ID PRTC_MOUSE STANDARD; PRT; 460 AA.
AC P33567; O35498; O91WN8; Q99PC6;

```

```

DT 01-FEB-1994 (Rel. 28, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE Name=Proc;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RA Tada N., Sato M., Teujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein cDNA.";
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Korf I.;
RT "Complete sequence of UC72A01.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBAJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=2398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
FAhey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Genome and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 274-433 FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a

```


"Amino acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).

[5]

PROCESSING, AND CALCIUM-BINDING DATA.

MDLINE=83213513; PubMed=6304092;

RA Esmon N.L.; Debault L.E.; Esmon C.T.;

RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C.";

RT domainless protein C.";

J. Biol. Chem. 258:5548-5553(1983).

[6]

PROCESSING, AND CALCIUM-BINDING DATA.

MDLINE=83213514; PubMed=6406503;

RA Johnson A.E.; Esmon N.L.; Laue T.M.; Esmon C.T.;

RT "Structural changes required for activation of protein C are induced by Ca2+ binding to a high affinity site that does not contain gamma-carboxyglutamic acid.";

RT carboxyglutamic acid.";

J. Biol. Chem. 258:5554-5560(1983).

CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

CC -!- SIMILARITY: Belongs to the peptidase S1 family.

CC -!- SIMILARITY: Contains 2 EGF-like domains.

CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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EMBL; K02435; AAA30685.1; -.

PIR; A26250; KXBO.

HSSP; P04070; 1AUT.

DR MEROPS; S01.218; -.

DR InterPro; IPR000152; Asx hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS50998; GLA_2; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Calcium-binding; Direct protein sequencing;

KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;

KW Hydroxylation; Repeat; Serine protease; Signal; Vitamin K.

FT NON_TER 1

FT SIGNAL <1 29

FT PROPEP 30 39

FT CHAIN 40 456

FT CHAIN 40 194

FT CHAIN 197 456

FT PEPTIDE 197 210

FT DOMAIN 40 85

FT DOMAIN 94 129

FT DOMAIN 133 173

FT DOMAIN 211 456

FT MOD_RES 45 45

FT MOD_RES 46 46

FT MOD_RES 53 53

FT MOD_RES 55 55

FT MOD_RES 58 58

FT MOD_RES 59 59

FT MOD_RES 62 62

FT MOD_RES 64 64

FT MOD_RES 65 65

FT MOD_RES 68 68

FT MOD_RES 74 74

FT MOD_RES 110 110

FT ACT_SITE 252 252

FT ACT_SITE 298 298

FT ACT_SITE 397 397

FT DISULFID 56 61

FT DISULFID 89 108

FT DISULFID 98 103

FT DISULFID 102 117

FT DISULFID 119 128

FT DISULFID 137 148

FT DISULFID 144 157

FT DISULFID 159 172

FT DISULFID 180 318

FT DISULFID 237 253

FT DISULFID 368 382

FT DISULFID 393 421

FT CARBOHYD 136 136

FT CARBOHYD 289 289

FT CARBOHYD 350 350

FT CARBOHYD 366 366

FT VARIANT 82 82

FT CONFLICT 455 456

FT SEQUENCE 456 AA; 51407 MW; CAA6F833F894C209 CRC64;

Query Match 54.2%; Score 104; DB 1; Length 456;

Best Local Similarity 45.5%; Pred. No. 8e-10;

Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRPGSLXRCXXQCFSXXARXIFKDXRTKLFWSY 44

Db 40 ANSFLEELRPGNVERECSEVCEFEAREIFQNTEDTMAFWSPY 83

RESULT 10

Q8JHC9 PRELIMINARY; PRT; 443 AA.

AC Q8JHC9; (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Coagulation factor VIII.
GN Name=f1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Hanumanthiah R., Day K., Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIII.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF519546; RAM88142.1; -;
DR EMBL; AF515269; AAN71000.1; -;
DR HSSP; P00740; ICFH.
DR ZFIN; ZDB-GENE-021206-10; f71.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS00011; GLA 1; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;

Query Match 53.1%; Score 102; DB 2; Length 443;
Best Local Similarity 41.9%; Pred. No. 1.8e-09;
Matches 18; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Ds 2 NAFLLXRPGLXKXKXQCSFXXARXIFDAXRTKLFWSY 44
40 SGFLEMKAGNLERECVEIEICDYEARVEFDDRTKQFWLSY 82

RESULT 11
ID FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor) (Stuart-
DE Power factor).
GN Name=F10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91216473; PubMed=1902434; DOI=10.1016/0378-1119(91)90141-W;
RX Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=87026600; PubMed=3768336;
RX Letys S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
RT organization is essentially identical with that of factor IX and
RT protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RX Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-
RT PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human blood
RT coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [6]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86221713; PubMed=3011603; DOI=10.1016/0378-1119(86)90112-5;
RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
RT "Isolation and characterization of human blood-coagulation factor X
RT cDNA.";
RL Gene 41:311-314(1986).
RN [7]
RP SEQUENCE OF 41-179
RX MEDLINE=83257207; PubMed=6871167;
RA McMullen B.A., Fujikawa K., Kistel W., Sasagawa T., Howald W.N.,
RA Kwa E.Y., Weinstein B.;
RT "Complete amino acid sequence of the light chain of human blood
RT coagulation factor X: evidence for identification of residue 63 as
RT beta-hydroxyaspartic acid.";
RL Biochemistry 22:2875-2884(1983).
RN [8]

into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-!- PTW: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

-!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

-!- SIMILARITY: Belongs to the peptidase S1 family.

-!- SIMILARITY: Contains 2 EGF-like domains.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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EMBL; X64336; CAA45617.1; -.
 PIR; S18994; S18994.
 HSSP; P04070; LAUT.
 MEROPS; S01.218; -.
 RGD; 3411; PROC
 InterPro; IPR000152; Asx_hydroxyl_S.
 InterPro; IPR000742; EGF 2.
 InterPro; IPR001881; EGF CA.
 InterPro; IPR006209; EGF like.
 InterPro; IPR002383; GLA_blood.
 InterPro; IPR009003; Pept_Ser_Cys.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR00294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; Gla; 1.
 Pfam; PF00089; Trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00179; EGF CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_SPC; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF 2; 2.
 PROSITE; PS00026; EGF 3; 1.
 PROSITE; PS01187; EGF CA; 1.
 PROSITE; PS00011; GLA_1; 1.
 PROSITE; PS00998; GLA_2; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Blood coagulation; Calcium-binding; EGF-like domain;
 Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 Repeat; Serine protease; Signal; Vitamin K.
 SIGNAL 1 32 By similarity.
 PROPEP 33 41 Vitamin K-dependent protein C.
 CHAIN 42 461 Vitamin K-dependent protein C light chain
 CHAIN 42 196 (By similarity).
 CHAIN 199 461 Vitamin K-dependent protein C heavy chain
 CHAIN 199 461 (By similarity).
 PEPTIDE 199 212 Activation peptide (By similarity).
 DOMAIN 42 87 Gla.
 DOMAIN 96 131 EGF-like 1.
 DOMAIN 135 175 EGF-like 2.
 DOMAIN 213 461 Serine protease.
 SITE 212 213 Cleavage (by thrombin) (By similarity).

FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE 254 254 Charge relay system.
 FT ACT_SITE 300 300 Charge relay system.
 FT ACT_SITE 402 402 Charge relay system.
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 110 By similarity.
 FT DISULFID 100 105 By similarity.
 FT DISULFID 104 119 By similarity.
 FT DISULFID 121 130 By similarity.
 FT DISULFID 139 150 By similarity.
 FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 320 Interchain (By similarity).
 FT DISULFID 239 255 By similarity.
 FT DISULFID 373 387 By similarity.
 FT DISULFID 398 426 By similarity.
 FT CARBOHYD 215 215 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;

Query Match 52.1%; Score 100; DB 1; Length 461;

Best Local Similarity 45.5%; Pred. No. 4.3e-09;

Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXCKXQCSPXXARXIPKDXRTKLFWSY 44

Db 42 ANSPLEVRAGSLRECMWEICDFEEAQEPQNVEDTLAFWKY 85

RESULT 15

Q68FY8

ID Q68FY8 PRELIMINARY; PRT; 461 AA.

AC Q68FY8;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Protein C.

GN Name:Proc.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL: BC078879; AAH78879.1; -
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase_S1.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 1.
DR Pfam: PF00594; Gla; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLA_1; UNKNOWN_1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1_
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 461 AA; 51826 MW; C0181CED046B584B CRC64;

Query Match 52.1%; Score 100; DB 2; Length 461;
Best Local Similarity 45.5%; Pred. No. 4.3e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXCXQCSPFXARXIFPKDAXTKLFWISY 44
Db 42 ANSFLEEVRAQSLRECMEEICDFEEAQEIFQNVEDTLAFWKY 85

Search completed: August 22, 2005, 09:36:14
Job time : 176 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:52 ; Search time 43 Seconds
(without alignments)
76.385 Million cell updates/sec

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFXXLRPGSLRXCKXKX.....XXARXIFKDAARTKLFWISY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	44	3	US-08-955-636-3
2	172	89.6	44	4	US-09-302-239-3
3	172	89.6	44	4	US-09-497-591-3
4	172	89.6	44	4	US-09-803-810-3
5	172	89.6	406	1	US-08-293-778-24
6	172	89.6	406	1	US-08-295-411-5
7	172	89.6	406	2	US-08-955-471-5
8	172	89.6	406	4	US-09-782-587B-1
9	172	89.6	406	4	US-09-782-587B-3
10	172	89.6	406	5	PCT-US92-10242-5
11	172	89.6	444	1	US-08-475-845-2
12	172	89.6	444	2	US-08-327-690-2
13	172	89.6	444	2	US-08-660-289-2
14	172	89.6	444	2	US-08-537-807-2
15	172	89.6	444	2	US-08-871-003-2
16	172	89.6	444	3	US-08-464-233-2
17	172	89.6	444	3	US-09-189-607-2
18	172	89.6	444	3	US-09-378-907-2
19	172	89.6	444	5	PCT-US94-05779-2
20	172	89.6	461	4	US-09-949-016-8839
21	172	89.6	466	1	US-07-882-202A-4
22	172	89.6	466	1	US-08-021-615A-4
23	172	89.6	466	1	US-08-321-777-4
24	172	89.6	466	3	US-09-009-217-14
25	172	89.6	466	3	US-09-009-656-14
26	172	89.6	466	5	PCT-US93-04493-4
27	172	89.6	483	4	US-09-949-016-9523

28	166	86.5	44	3	US-08-955-636-29	Sequence 29, Appl
29	164	85.4	44	3	US-08-955-636-26	Sequence 26, Appl
30	164	85.4	44	3	US-08-955-636-27	Sequence 27, Appl
31	164	85.4	44	3	US-08-955-636-28	Sequence 28, Appl
32	160	83.3	44	3	US-08-955-636-30	Sequence 30, Appl
33	157	81.8	41	1	US-08-229-280-4	Sequence 4, Appl
34	152	79.2	42	4	US-09-383-667-7	Sequence 7, Appl
35	131	68.2	44	3	US-08-955-636-4	Sequence 4, Appl
36	131	68.2	44	4	US-09-302-239-4	Sequence 4, Appl
37	131	68.2	44	4	US-09-497-591-4	Sequence 4, Appl
38	131	68.2	44	4	US-09-803-810-4	Sequence 4, Appl
39	111	57.8	139	1	US-08-330-978-2	Sequence 2, Appl
40	111	57.8	139	1	US-08-474-042-2	Sequence 2, Appl
41	111	57.8	139	1	US-08-484-558-2	Sequence 2, Appl
42	111	57.8	139	1	US-08-774-592-2	Sequence 2, Appl
43	111	57.8	437	1	US-08-487-037-2	Sequence 2, Appl
44	111	57.8	437	1	US-08-487-037-3	Sequence 3, Appl
45	111	57.8	488	1	US-08-487-037-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955.636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match	89.6%	Score 172;	DB 3;	Length 44;
Best Local Similarity	100.0%	Pred. No. 1e-21;		
Matches	44;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	ANAFXXLRPGSLRXCKXKXCSFXXARXIFKDAARTKLFWISY	44	
Db	1	ANAFXXLRPGSLRXCKXKXCSFXXARXIFKDAARTKLFWISY	44	

RESULT 2
US-09-302-239-3
; Sequence 3, Application US/09302239
; Patent No. 6693075
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/302,239
; CURRENT FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44

RESULT 3
US-09-497-591-3
; Sequence 3, Application US/09497591
; Patent No. 6747003
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; EARLIER FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
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; LENGTH: 44
; TYPE: PRT
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; FEATURE:
; NAME/KEY: MOD_RES
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; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44

RESULT 4
US-09-803-810-3
; Sequence 3, Application US/09803810
; Patent No. 6762286
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; EARLIER FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
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; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
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; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 89.6%; Score 172; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

Query Match 89.6%; Score 172; DB 1; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44
Db 1 ANAFLLXLRPGSLXRCXKXQCSPXXARXIFKDAKRTKLFWSY 44

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RESULT 6
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
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; US-08-295-411-5
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; Query Match 89.6%; Score 172; DB 1; Length 406;
; Best Local Similarity 77.3%; Pred. No. 1e-20;
; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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; RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; US-08-295-411-5
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; Query Match 89.6%; Score 172; DB 1; Length 406;
; Best Local Similarity 77.3%; Pred. No. 1e-20;
; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
;
; QY 1 ANAFLLXLRPGSLXRXCKXQCSFXXARXIFKDAERTKLFWISY 44
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; DB 1 ANAFLEELRPGSLERCKEKEQCSFEAREIFKDAERTKLFWISY 44
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; RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
;
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; US-08-955-471-5
;
; Query Match 89.6%; Score 172; DB 2; Length 406;
; Best Local Similarity 77.3%; Pred. No. 1e-20;
; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
;
; QY 1 ANAFLLXLRPGSLXRXCKXQCSFXXARXIFKDAERTKLFWISY 44
; | | | | | | | | | | | | | | | | | | | | | | | |
; DB 1 ANAFLEELRPGSLERCKEKEQCSFEAREIFKDAERTKLFWISY 44
; | | | | | | | | | | | | | | | | | | | | | | | |
;
; RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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;; PRIOR APPLICATION NUMBER: PA 2000 00218
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: 60/184,036
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/241,916
;; PRIOR FILING DATE: 2000-10-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)-(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)-(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)-(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match 89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
Db 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44

RESULT 9
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match 89.6%; Score 172; DB 4; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
Db 1 ANAFLELRPGSLRECKEQCSFEEARIFKDAERTKLFWISY 44
RESULT 10
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Meesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10242
; FILING DATE: 19921118
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRO472P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 89.6%; Score 172; DB 5; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRPGSLRXKXKXQCSFXXARXIFKDAERTKLFWISY 44
Db 1 ANAFLELRPGSLRECKEQCSFEEARIFKDAERTKLFWISY 44

RESULT 11
US-08-475-845-2

; Sequence 2, Application US/08475845
; Patent No. 5788965

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,845

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/327,690

; FILING DATE: 24-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/065,725

; FILING DATE: 21-MAY-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/662,920

; FILING DATE: 28-FEB-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCES/DOCKET NUMBER: 13952-8-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-467-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 444 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-475-845-2

Query Match 89.6%; Score 172; DB 1; Length 444;

Best Local Similarity 77.3%; Pred. No. 1.1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQCSFXAXRIFKDAERTKLFWISY 44

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Db 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12

US-08-327-690-2

; Sequence 2, Application US/08327690

; Patent No. 5817788

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/327,690

; FILING DATE: 24-OCT-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/065,725

; FILING DATE: 21-MAY-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/662,920

; FILING DATE: 28-FEB-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCES/DOCKET NUMBER: 13952-8-3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-467-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 444 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-327-690-2

Query Match 89.6%; Score 172; DB 2; Length 444;

Best Local Similarity 77.3%; Pred. No. 1.1e-20;

Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ANAFLLXLRPGSLRXKXQCSFXAXRIFKDAERTKLFWISY 44

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13

US-08-660-289-2

; Sequence 2, Application US/08660289

; Patent No. 5833982

; GENERAL INFORMATION:

; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus

; TITLE OF INVENTION: Modified Factor VII

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94105-1492

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAFLLXLRPGSLRXCKXQCSCFXXARXIFKDXRTKLFWISY 44
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAFLLXLRPGSLRXCKXQCSCFXXARXIFKDXRTKLFWISY 44
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-003-2

Query Match      89.6%; Score 172; DB 2; Length 444;
Best Local Similarity 77.3%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAFLLXLRPGSLRXCKXQCSCFXXARXIFKDXRTKLFWISY 44
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Db 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: August 22, 2005, 09:37:01
Job time : 44 secs
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1	172	89.6	44	9	US-09-803-810-3	Sequence 3, Appli
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3	172	89.6	44	16	US-09-855-068-3	Sequence 3, Appli
4	172	89.6	406	10	US-09-782-587B-1	Sequence 1, Appli
5	172	89.6	406	10	US-09-782-587B-3	Sequence 3, Appli
6	172	89.6	406	14	US-10-109-498-1	Sequence 1, Appli
7	172	89.6	406	14	US-10-255-032-1	Sequence 1, Appli
8	172	89.6	406	14	US-10-281-727-1	Sequence 1, Appli
9	172	89.6	406	15	US-10-386-898-7	Sequence 7, Appli
10	172	89.6	406	15	US-10-383-898-1	Sequence 1, Appli
11	172	89.6	406	15	US-10-617-500-1	Sequence 1, Appli


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match      89.6%; Score 172; DB 10; Length 406;
Best Local Similarity 77.3%; Pred. No. 5.3e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44
Db 1 ANAFLEELRPGSLRECKEQSFPEARIFKDXARTKLFWISY 44

RESULT 6
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44

RESULT 7
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A1o No. US20030100075Aldisk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
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US-10-255-032-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44

RESULT 8
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1

Query Match      89.6%; Score 172; DB 14; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44
Db 1 ANAFLXLRPGSLRXCKXQCXSFXXARXIFKDXARTKLFWISY 44

RESULT 9
US-10-386-898-7
; Sequence 7, Application US/10386898
; Publication No. US20030229018A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030229018A1o No. US20030229018Aldisk Pharmaceuticals, Inc.
; APPLICANT: Kjalke, Marianne
; APPLICANT: Jakobsen, Palle
; APPLICANT: Stennicke, Henning Ralf
; TITLE OF INVENTION: DIMERIC TF ANTAGONIST
; FILE REFERENCE: 6445.200-US
; CURRENT APPLICATION NUMBER: US/10/386,898
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/365,935
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
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; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-386-898-7

Query Match	89.6%	Score 172;	DB 15;	Length 406;
Best Local Similarity	100.0%	Pred. No. 5.3e-21;		
Matches 44;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1 ANAFXXLRPGSLRXCXOXCFFXARXIFKDAXRTKLFWISY 44
D6	1 ANAFXXLRPGSLRXCXOXCFFXARXIFKDAXRTKLFWISY 44

```

RESULT 10
US-10-383-898-1
; Sequence 1, Application US/10383898
; Publication No. US20040009914A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Curcuminoid-protein conjugates
; FILE REFERENCE: E056 1060.1
; CURRENT APPLICATION NUMBER: US/10/383,898
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(406)
US-10-383-898-1

```

Query Match 89.6%; Score 172; DB 15; Length 406;
Best Local Similarity 77.3%; Pred. No. 5.3e-21;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	ANAFLLXLRPGSLXRXCXXQCXFXXARXIFKDAERTKLFWISY	44
Db	1	ANAFLEELRPGSLERECKEEOCFEAREIFKDAERTKLFWISY	44

```

RESULT 11
US-10-617-500-1
; Sequence 1, Application US/10617500
; Publication No. US20040072755A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Stennicke, Henning R
; APPLICANT: Bjorn, Soren E
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: TF Antagonist
; FILE REFERENCE: 6510.200-US
; CURRENT APPLICATION NUMBER: US/10/617,500
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,567
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxy)
US-10-617-500-1

```

Query Match 89.6%; Score 172; DB 15; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels

[illegible]

```

RESULT 12
US-10-263-205B-2
; Sequence 2, Application US/10263205B
; Publication No. US20040087498A1
; GENERAL INFORMATION:
; APPLICANT: BERKNER, Kathleen L.
; APPLICANT: PETERSEN, Lars
; APPLICANT: HART, Charles E.
; APPLICANT: HEDNER, Ulla
; APPLICANT: BREGENGAARD, Claus
; TITLE OF INVENTION: MODIFIED FACTOR VII
; FILE REFERENCE: 13952N-8-5-1
; CURRENT APPLICATION NUMBER: US/10/263,205B
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/464,029
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/327,690
; PRIOR FILING DATE: 1994-10-24
; PRIOR APPLICATION NUMBER: PCT/US94/05779
; PRIOR FILING DATE: 1994-05-23
; PRIOR APPLICATION NUMBER: 08/065,725
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: PCT/US92/01636
; PRIOR FILING DATE: 1991-02-28
; PRIOR APPLICATION NUMBER: 07/662,920
; PRIOR FILING DATE: 1991-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-205B-2

```

Query Match 89.6%; Score 172; DB 15; Length 406;
Best Local Similarity 77.3%; Pred. No. 5.3e-21;
Matches 34: Conservative 0; Mismatches 10; Indels

```
QY 1 ANAFLLXLRPGSLXRXCXXQCSPXXARXIFKDAXRKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
db 1 ANAFLEELRPGSLERECKEEQCSFEERAREIFKDAERTKLFWISY 44
```

```

RESULT 13
US-10-617-619-1
; Sequence 1, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 010991
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PR

```

```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; TYPE: PRT
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
Db 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
```

RESULT 14

```
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication No. US20040143099A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jakob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; TITLE OF INVENTION: and a Blood Glucose Regulator
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
Db 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
```

RESULT 15

```
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication No. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1
```

```
Query Match      89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
Db 1 ANAFLXLLRPGSLRXKXXQCXXCFXXARXIFKDAARTKLFWISY 44
```

Search completed: August 22, 2005, 09:55:12
Job time : 160 secs

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Query Match 81.6%; Score 161.5; DB 2; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 2
AAB36395
ID AAB36395 standard; peptide; 44 AA.
AC AAB36395;
XX
XX 27-FEB-2001 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
KW clotting disorder; haemophilia A; haemophilia B; liver disease.
XX
XX Homo sapiens.
OS
XX WO20066753-A2.
FN
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US011416.
XX
XX 29-APR-1999; 99US-00302239.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Nelsetuen GL;
PI
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified gamma-
PT carboxy glutamic acid domain that enhances membrane binding affinity.
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having at
CC least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation. (I)
CC can have thrombolytic and haemostatic activities, and can be used as an
CC inhibitor of clot formation. (II) is useful for decreasing clot formation
CC in a mammal, a factor VII or factor IX containing a modified GLA domain
CC is useful for increasing clot formation and for treating a bleeding
CC disorder, including thrombosis and clotting disorders such as haemophilia
CC A, haemophilia B and liver disease. The present sequence represents a
CC wild type human factor VII GLA domain sequence, given in the
CC exemplification of the present invention
XX
XX Sequence 44 AA;
SQ

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 3
ADD50096
ID ADD50096 standard; protein; 44 AA.
XX
XX ADD50096;
AC
XX 15-JAN-2004 (first entry)
XX
XX Human vitamin K-dependent protein #2.
XX
XX Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
KW GLA domain; membrane binding affinity; clot formation; haemophilia;
KW clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
KW thrombolytic.
XX
XX Homo sapiens.
OS
XX US2003100506-A1.
FN
XX 29-MAY-2003.
XX
XX 18-NOV-2002; 2002US-00298330.
XX
XX 23-OCT-1997; 97US-00955636.
PR 29-APR-1999; 99US-00302239.
XX 03-FEB-2000; 2000US-00497591.
XX
XX (NELS/) NELSESTUEN G L.
PA
XX Nelsetuen GL;
PI
XX WPI; 2003-606646/57.
XX
XX New vitamin K-dependent polypeptide for modulating clot formation in
PT mammals comprises a modified gamma-carboxyglutamic acid domain that
PT enhances membrane binding affinity and activity of the polypeptide.
XX
XX Example 5; SEQ ID NO 3; 51pp; English.
XX
XX The invention relates to a vitamin K-dependent polypeptide comprising a
CC modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane
CC binding affinity and activity of the polypeptide relative to a
CC corresponding native vitamin K-dependent polypeptide, where the modified
CC GLA domain comprises a glutamic acid residue at position 34. The
CC polypeptide is useful in modulating clot formation in mammals or in
CC treating certain types of haemophilia or clotting disorders. The membrane
CC binding affinity of polypeptides is increased by site directed
CC mutagenesis in the GLA domain. This sequence represents a vitamin K-
CC dependent protein of the invention.
XX
XX Sequence 44 AA;
SQ

Query Match 81.6%; Score 161.5; DB 7; Length 44;
Best Local Similarity 97.8%; Pred. No. 6.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRCXKXQCXFXXARXIFKDXRTKLFWISY 44

RESULT 4
ADQ26902
ID ADQ26902 standard; protein; 44 AA.
XX
XX ADQ26902;
AC
XX 26-AUG-2004 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid (GLA) domain.
XX
XX Human; clot formation; protein C; activated protein C; APC;
KW gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;
KW

KW aspirin; warfarin; heparin; haemophilic disorder; haemostatic;
 KW anticoagulant; factor VII.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 1. .44
 FT /label= OTHER
 FT /note= "OTHER= All Xaa residues are glutamic acid or
 FT gamma carboxyglutamic acid"
 XX
 XX
 PN US6747003-B1.
 XX
 XX PD 08-JUN-2004.
 XX
 XX PF 03-FEB-2000; 2000US-00497591.
 XX
 XX PR 23-OCT-1997; 97US-00955636.
 XX PR 29-APR-1999; 99US-00302239.
 XX
 XX (MINU) UNIV MINNESOTA.
 PA Nelsestuen GL;
 XX
 XX WIPI; 2004-429803/40.
 DR
 XX
 XX Decreasing clot formation by administering an anticoagulant agent, and a
 PT protein C or activated protein C polypeptide having a modified GLA
 PT domain, useful for treating hemophilic disorders in mammals.
 XX
 XX Example 5; SEQ ID NO 3; 4lpp; English.
 XX
 XX The invention relates to a method of decreasing clot formation comprising
 CC administering to a patient an anticoagulant agent and a protein C or
 CC activated protein C (APC) polypeptide comprising a modified gamma-
 CC carboxyglutamic acid (GLA) domain with two, three, four or five amino
 CC acid substitutions. The invention also relates to vitamin K-dependent
 CC nucleic acids, polypeptides, host cells, vectors and antibodies used in
 CC the methods of the invention. The anticoagulant agent is aspirin,
 CC warfarin or heparin, preferably aspirin. The methods and compositions of
 CC the present invention are useful for modulating clot formation for
 CC treating haemophilic disorders in mammals. This sequence represents the
 CC human factor VII GLA domain, used in the method of the invention.
 XX
 SQ Sequence 44 AA;
 Query Match 81.6%; Score 161.5; DB 8; Length 44;
 Best Local Similarity 97.8%; Pred. No. 6.1e-20; Indels 1; Gaps 1;
 Matches 44; Conservative 0; Mismatches 0;
 QY 1 ANAGFLXXLRPGSLRXKCKXXQCSFXXARXIFKDAKRTKLFWISY 45
 DB 1 ANA-FLXXLRPGSLRXKCKXXQCSFXXARXIFKDAKRTKLFWISY 44
 XX
 RESULT 5
 AAB84870
 ID AAB84870 standard; protein; 401 AA.
 XX
 AC AAB84870;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-31).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

FT
 FT
 XX
 PN JP2001061479-A.
 XX
 PD 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX Claim 14; Page 20-21; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 401 AA;
 Query Match 81.6%; Score 161.5; DB 4; Length 401;
 Best Local Similarity 75.6%; Pred. No. 5.9e-19; Indels 1; Gaps 1;
 Matches 34; Conservative 0; Mismatches 10;
 QY 1 ANAGFLXXLRPGSLRXKCKXXQCSFXXARXIFKDAKRTKLFWISY 45
 DB 1 ANA-FLXXLRPGSLRXKCKXXQCSFXXARXIFKDAKRTKLFWISY 44
 XX
 RESULT 6
 AAB84871
 ID AAB84871 standard; protein; 401 AA.
 XX
 AC AAB84871;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-39).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 235. .239
 FT /note= "Wild-type Val-Pro-Gly-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 FT Misc-difference 311. .317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.

```

XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of haemophilia.
XX Claim 16; Page 23-24; 29pp; Japanese.
XX The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
CC agent for the substitution therapy of haemophilia inhibitor patients
XX
SQ Sequence 401 AA;
    Query Match      81.6%; Score 161.5; DB 4; Length 401;
    Best Local Similarity 75.6%; Pred. No. 5.9e-19;
    Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSPXXARXIFKDXRTKLFWISY 45
    ||| || ||||| || ||||| ||||| ||||| ||||| |||||
Db 1 ANA-FLLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 7
AAR35764
ID AAR35764 standard; protein; 406 AA.
XX AC AAR35764;
XX
XX 25-MAR-2003 (revised)
DT 24-SEP-1993 (first entry)
XX
XX Factor VII (VII).
XX
XX PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite;
KW catalytic activity.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..152 /note= "Factor VII light chain"
FT Region 153..406 /note= "Factor VII heavy chain"
FT Peptide 245..266 /note= "Claim 9, page 138-139 describes an antibody that
FT reacts with Factor VII; fragments 289-304, 290-304, 290-
FT 310, 374-388 and 400-414 but not with fragment 245-266"
FT Peptide 289..304 /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..310 /note= "exosite 2"
FT Peptide 290..310 /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 290..304 /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 374..388 /note= "exosite 1"
FT Peptide 374..388 /note= "pref. PC polypeptide; claim 2, page 136"
XX
XX WO9309804-A1.
PN
XX 27-MAY-1993.
PD
XX 18-NOV-1992; 92WO-US010242.
XX
XX 18-NOV-1991; 91US-00793989.
XX
XX (SCRI ) SCRIPPS RES INGT.
XX
XX Griffin JH, Meesters RM;
XX

```

```

DR WPI; 1993-182244/22.
XX Serine protease derived-polypeptide(s) and anti-peptide antibodies - for
PT inhibiting coagulation and assaying for the presence of serine protease
XX in fluid samples.
XX Disclosure; Page 133-135; 149pp; English.
XX The PC polypeptides indicated in the Features Table inhibit coagulation
CC (they prevent binding of serine protease to natural substrates), esp.
CC when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-
CC 10) microM. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are
CC described in the specification but have not yet been added to the
CC SEQUENCE LISTING. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 406 AA;
    Query Match      81.6%; Score 161.5; DB 2; Length 406;
    Best Local Similarity 75.6%; Pred. No. 6e-19;
    Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSPXXARXIFKDXRTKLFWISY 45
    ||| || ||||| || ||||| ||||| ||||| ||||| |||||
Db 1 ANA-FLLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
AAR14510
ID AAR14510 standard; protein; 406 AA.
XX AC AAR14510;
XX
XX 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
XX Modified blood coagulation Factor VII (R315S).
DE Blood coagulation; factor 7; mutein; mutation; modification;
KW thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 6 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 7 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 14 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 16 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Disulfide-bond 17..22 /label= OTHER
FT Modified-site 19 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 25 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33 /label= OTHER
FT /note= "gamma-carboxyglutamic acid"

```


FT	Modified-site	/note= "proteolytic site"	
FT		35	
FT		/label= OTHER	
FT	Cleavage-site	/note= "gamma-carboxyglutamic acid"	
FT		38. .39	
FT	Cleavage-site	/note= "proteolytic site"	
FT		42. .43	
FT	Cleavage-site	/note= "proteolytic site"	
FT		44. .45	
FT	Disulfide-bond	/note= "proteolytic site"	
FT		50. .61	
FT	Disulfide-bond	/note= "proteolytic site"	
FT		55. .70	
FT	Modified-site	63	
FT		/label= OTHER	
FT		/note= "beta-hydroxy-aspartic acid"	
FT		72. .81	
FT	Disulfide-bond	91. .102	
FT	Disulfide-bond	98. .112	
FT	Disulfide-bond	114. .127	
FT	Disulfide-bond	135. .162	
FT	Cleavage-site	143. .144	
FT		/note= "proteolytic site"	
FT	Modified-site	145	
FT		/note= "glycosylation site"	
FT	Disulfide-bond	159. .164	
FT	Disulfide-bond	178. .194	
FT	Active-site	193	
FT	Active-site	242	
FT	Cleavage-site	290. .291	
FT		/note= "proteolytic site"	
FT	Disulfide-bond	310. .329	
FT	Cleavage-site	315. .316	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	Misc-difference	315	
FT		/note= "naive Arg315 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT		322	
FT	Modified-site	/note= "glycosylation site"	
FT	Disulfide-bond	340. .368	
FT	Cleavage-site	341. .342	
FT		/note= "proteolytic site"	
FT	Active-site	344	
FT	Cleavage-site	392. .393	
FT		/note= "proteolytic site"	
FT	Cleavage-site	396. .397	
FT		/note= "proteolytic site"	
FT	Cleavage-site	402. .403	
FT		/note= "proteolytic site"	
XX		US5580560-A.	
XX		PN	
XX		03-DEC-1996.	
XX			
XX	22-AUG-1994;	94US-00293778.	
XX			
PR	13-NOV-1989;	89US-00434149.	
PR	12-JUN-1992;	92US-00898248.	
PR	09-AUG-1993;	93US-00104509.	
XX			
XX	(NOVO) NOVO-NORDISK AS.		
XX			
XX			
PI	Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;		
XX			
XX	WPT; 1997-033523/03.		
XX			
XX	Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability.		
XX			
PS	Example 4; Page; 28pp; English.		
XX			
CC	Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys38, Lys38, Ile642, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an		
CC			

CC	amino acid that provides a proteolytically more stable peptidic
CC	provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala
CC	The modified proteins are useful for treating bleeding disorders
CC	thrombocytopenia and von Willebrand's disease. They are also a
CC	addition to plasma substitutes. The present sequence is a spec
CC	example of a modified factor VII protein.. (Updated on 25-MAR-2
CC	correct PF field.)
XX	
SQ	Sequence 406 AA;
	Query Match 81.6%; Score 161.5; DB 2; Length 406;
	Best Local Similarity 75.6%; Pred. No. 6e-19;
	Matches 34; Conservative 0; Mismatches 10; Indels 1
Oy	1 ANAGFLXLLRPGSLXRXCXXQCSPXXAXRIFKDAERTKLFWISY 45
Db	1 ANA-FLELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 9	
AAW14509	ID AAW14509 standard; protein; 406 AA.
XX	AC AAW14509;
XX	
DT	25-MAR-2003 (revised)
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (R290S).
XX	
KW	Blood coagulation; factor 7; mutein; mutation; modification;
KW	thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 6 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 7 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 14 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 16 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Disulfide-bond 17..22 /label= OTHER
FT	Modified-site 19 /note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 20 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 25 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 26 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Modified-site 29 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site 32..33 /label= OTHER
FT	/note= "proteolytic site"
FT	
FT	Modified-site 35 /label= OTHER
FT	/note= "gamma-carboxyglutamic acid"
FT	
FT	Cleavage-site 38..39 /label= OTHER
FT	/note= "proteolytic site"
FT	
FT	Cleavage-site 42..43 /label= OTHER
FT	/note= "proteolytic site"

ID	AAB84868	standard; protein; 406 AA.
XX		
XX		
FT	Misc-difference	235..239
FT	/note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-	

FT Arg-Lys-Thr-Leu"
 PN JP2001061479-A.
 XX 13-MAR-2001.
 PD
 XX 24-AUG-1999; 99JP-00237610.
 PF
 XX 24-AUG-1999; 99JP-00237610.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX Claim 9; Page 17-18; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.6%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 6e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 DB 1 ANAGFLXXLRPGSLRXCKXXQCSPFXAXRIFKDXRTKLFWISY 45
 1 ANA-FLEELRPGSLRECKEQCFEAREIFKDAERTKLFWISY 44
 RESULT 14
 ID AAB84866 standard; protein; 406 AA.
 AC AAB84866;
 XX
 XX 31-JUL-2001 (first entry)
 DT
 XX Wild-type human blood coagulant factor VII (FVII).
 DE
 XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 159..164
 FT
 XX JP2001061479-A.
 PN
 XX 13-MAR-2001.
 PD
 XX 24-AUG-1999; 99JP-00237610.
 PF
 XX 24-AUG-1999; 99JP-00237610.
 PR
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 PA
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19459.
 XX
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 PT
 XX Disclosure; Page 8-9; 29pp; Japanese.
 PS
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present

CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 SQ Sequence 406 AA;
 Query Match 81.6%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 6e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 DB 1 ANAGFLXXLRPGSLRXCKXXQCSPFXAXRIFKDXRTKLFWISY 45
 1 ANA-FLEELRPGSLRECKEQCFEAREIFKDAERTKLFWISY 44
 RESULT 15
 ID AAM52183 standard; protein; 406 AA.
 AC AAM52183;
 XX
 XX 07-FEB-2002 (first entry)
 DT
 XX Human FVII mutant V253N.
 DE
 XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutuin.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 6 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 7 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 14 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 16 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 19 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 20 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 25 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 26 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 29 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Misc-difference 35 /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT
 FT Modified-site 52 /note= "O-glycosylated"
 FT
 FT Modified-site 60 /note= "O-glycosylated"
 FT
 FT Modified-site 145 /note= "N-glycosylated"
 FT
 FT Cleavage-site 152..153 /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains linked by a

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 25 Seconds
(without alignments)
173.190 Million cell updates/sec

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANAGFLXXLRPGSLRXCKX.....XXARXIFKQAXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.6	466	1 KFHU7	coagulation factor
2	127.5	64.4	443	2 I46932	coagulation factor
3	119	60.1	407	1 KFB07	coagulation factor
4	98.5	49.7	461	1 JX0210	protein C (activat
5	95	48.0	617	2 S10511	thrombin (EC 3.4.2
6	95	48.0	618	2 A35827	thrombin (EC 3.4.2
7	93.5	47.2	456	1 KXBO	protein C (activat
8	93	47.0	416	1 KFB0	coagulation factor
9	91.5	46.2	488	1 EXHU	coagulation factor
10	91	46.0	461	1 KFHU	coagulation factor
11	90.5	45.7	492	1 EXBO	coagulation factor
12	89.5	45.2	461	1 S18994	protein C (activat
13	85.5	43.2	482	1 EXRT	coagulation factor
14	85	42.9	452	1 A30351	coagulation factor
15	85	42.9	459	2 J00419	coagulation factor
16	80.5	40.7	475	1 EXCH	coagulation factor
17	78	39.4	625	1 TBBO	thrombin (EC 3.4.2
18	73.5	37.1	461	1 KXHU	protein C (activat
19	73	36.9	622	1 TBHU	thrombin (EC 3.4.2
20	65	32.8	396	1 KXBOZ	plasma protein Z -
21	61.5	31.1	576	2 G96763	probable MAP kinase
22	60	30.3	422	1 KXHUZ	plasma protein Z p
23	58.5	29.5	642	2 S34333	plasma protein S p
24	57.5	29.0	594	2 D84859	probable MAP kinase
25	57.5	29.0	603	2 C96575	probable MAP kinase
26	56	28.3	675	1 KXBOS	plasma protein S p
27	55	27.8	673	2 A48089	growth arrest-spec
28	53.5	27.0	642	2 S3434	plasma protein S p
29	53.5	27.0	646	2 S38819	plasma protein S -

ALIGNMENTS

RESULT 1

KFHU7

coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004

C:Accession: A28322; A23819; A31186; B31186; S63524

R:O'Hara, P. J.; Grant, F. J.; Haldeman, B. A.; Gray, C. L.; Insley, M. Y.; Hagen, F. S.; Murri

Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987

A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende

A:Reference number: A28322; MUID:87260948; PMID:3037537

A:Accession: A28322

A:Molecule type: DNA

A:Residues: 1-466 <OHA>

A:Cross-references: UNIPROT:P08709; GB:J02933; NID:G180333; PIDN:AAA51983.1; PID:G180334

R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C

Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986

A:Title: Characterization of a cDNA coding for human factor VII.

A:Reference number: A23819; MUID:86205965; PMID:3486420

A:Accession: A23819

A:Molecule type: mRNA

A:Residues: 1-466 <HAG>

A:Cross-references: GB:M13232; NID:G182799; PIDN:AAA88040.1; PID:G182801

R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F

Biochemistry 27, 7785-7793, 1988

A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f

A:Reference number: A90539; MUID:89088153; PMID:3264725

A:Accession: A31186

A:Molecule type: protein

A:Residues: 61-212 <THI>

A:Accession: B31186

A:Molecule type: protein

A:Residues: 213-466 <TH2>

R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders

J. Biol. Chem. 266, 11051-11057, 1991

A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at

A:Reference number: A40529; MUID:91250411; PMID:1904059

A:Contents: annotation; carbohydrate binding sites

R:Persson, E.; Petersen, L.C.

Eur. J. Biochem. 234, 293-300, 1995

A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy

A:Reference number: S63524; MUID:96096752; PMID:8529655

A:Accession: S63524

A:Molecule type: protein

A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>

C:Genetics:

A:Gene: GDB:F7

A:Cross-references: GDB:119897; OMIM:227500

A:Map position: 13q34-13q34

A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

coagulation factor IX in the presence of calcium and tissue factor

FIG. 1. *Hydroxyaspartic acid in vitamin K-dependent protein C.*
 A: Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A: Reference number: A19316; MUID: 83169769; PMID: 6572939
 A: Contents: annotation: revision to residue 110
 A: Contents: annotation: revision to residue 110
 FIG. 1. *Hydroxyaspartic acid in vitamin K-dependent protein C.*
 A: Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A: Reference number: A19316; MUID: 83169769; PMID: 6572939
 A: Contents: annotation: revision to residue 110
 A: Contents: annotation: revision to residue 110

F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-234/Domain: activation peptide #status experimental <APT>
F;235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
F;57-62/Diulfide bonds: #status Predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/179/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;103/Modified site: carbohydurate (Thr) (covalent) #status experimental
F;199,211/Binding site: carbohydurate (Asn) (covalent) #status experimental
F;231,231/Binding site: carbohydurate (Asn) (covalent) #status experimental
F;234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 46.2%; Score 91.5; DB 1; Length 488;
Best Local Similarity 40.0%; Pred. NO. 2.1e-07;
Matches 18; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 ANAGFLXLRPGSLRXKCKXQCSFXXARXIFKDAKXRTKLFWISY 45
41 ANS-FLEMKKGLHRECMETCSYEAREVFEDSKTNEFWNKY 84

Db

RESULT 10

KFHU

Coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N;Alternate names: antihemophilic factor B; Christmas factor
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A207
R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3735-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A;Reference number: A00922; MUID:86000558; PMID:2994716
A;Accession: A00922
A;Molecule type: DNA
A;Residues: 1-461 <VOS>
A;Cross-references: UNIPROT:P00740; GB:K02402; NID:gl82612; PIDN:AAB59620.1; PID:gl82613
R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Brown
EMBO J. 3, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:84236100; PMID:6329734
A;Accession: A37570
A;Molecule type: DNA
A;Residues: 1-461 <ANS>
R;Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
A;Reference number: A30511; MUID:88327116; PMID:3416069
A;Accession: A30511
A;Molecule type: DNA
A;Residues: 8-24 <REI>
A;Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
R;Koerber, D.D.; Bortema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am. J. Hum. Genet. 45, 448-457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymor
A;Reference number: A32989; MUID:89371752; PMID:2773937
A;Accession: A32989
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 30-92 <KOE>
R;McGraw, R.A.; Davits, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulati
A;Reference number: A22673; MUID:85190593; PMID:3857619
A;Accession: A22673
A;Molecule type: mRNA
A;Residues: 1-193,'T',195-461 <MCG>

A;Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A;Note: the authors translated the codon ACA for residue 29 as TYR
R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findel, A.; Tolstosh
Nucleic Acids Res. 11, 2325-2335, 1983
A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A;Reference number: A21337; MUID:83220788; PMID:6687940
A;Accession: A21337
A;Molecule type: mRNA
A;Residues: 1-193, 'T', 195-461 <JAY>
A;Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611
R;Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A;Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A;Reference number: A37546; MUID:84300526; PMID:6089357
A;Accession: A37546
A;Molecule type: mRNA
A;Residues: 38-193, 'T', 195-326 <JAG>
A;Cross-references: GB:M35672
R;Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A;Title: Isolation and characterization of a cDNA coding for human factor IX.
A;Reference number: A30623; MUID:83065193; PMID:6959130
A;Accession: A30623
A;Molecule type: mRNA
A;Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',
A;Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
A;Experimental source: liver
R;Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A;Title: Development of an immunoaffinity process for factor IX purification.
A;Reference number: A60486; MUID:90194857; PMID:2316207
A;Accession: A60486
A;Molecule type: protein
A;Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65, 65 <THA>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: A20274
A;Molecule type: protein
A;Residues: 105-109, 'X', 111-115 <MCW>
R;Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
Eur. J. Biochem. 172, 565-572, 1988
A;Title: Characterisation of two differently processed forms of human recombinant factor
A;Reference number: S02527; MUID:88166735; PMID:3280312
A;Accession: S02527
A;Molecule type: protein
A;Residues: 29-63 <BAL>
A;Note: processed forms expressed in recombinant system
R;Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,
EMBO J. 9, 3295-3301, 1990
A;Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
A;Reference number: S12058; MUID:91006024; PMID:2209546
A;Accession: S12058
A;Molecule type: mRNA; protein
A;Residues: 1-68 <JAL>
A;Note: processed forms expressed in recombinant system
R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
EMBO J. 9, 475-480, 1990
A;Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
A;Reference number: S12377; MUID:90151623; PMID:2406129
A;Accession: S12377
A;Molecule type: protein
A;Residues: 92-130 <HAN>
A;Note: NMR detection of calcium binding by domain expressed in recombinant system
R;de la Salle, C.; Charmanlier, J.B.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunebaum,
Thromb. Haemost. 70, 370-371, 1993
A;Title: A deletion located in the 3' non translated part of the factor IX gene responsi
A;Reference number: I59612; MUID:94054330; PMID:8236150
A;Accession: I59612
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 444-461 <RES>

A;Cross-references: GB:S66752; NID:g439773; PIDN:AAB28588.1; PID:g439774
R;Stoflet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A;Title: Genomic amplification with transcript sequencing.
A;Reference number: I59529; MUID:88127096; PMID:3340835
A;Accession: I59529
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 230-359 <RE2>
A;Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623
R;Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iwa
Biochemistry 33, 5167-5171, 1994
A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically link
A;Reference number: A54255; MUID:94227047; PMID:8172892
A;Accession: A54255
A;Molecule type: protein
A;Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D' <AGH>
A;Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
R;Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
J. Clin. Invest. 61, 1528-1538, 1978
A;Title: Activation of human factor IX (Christmas factor).
A;Reference number: A18483; MUID:78194509; PMID:659613
A;Contents: annotation; activation; active site; carbohydrate binding
R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984
A;Reference number: A37569
A;Contents: annotation
A;Note: 194-thr was also found
R;Morita, T.; Isaacs, B.S.; Eamon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A;Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
A;Reference number: A37543; MUID:84185715; PMID:6425296
A;Contents: annotation; calcium binding
R;Morita, T.; Isaacs, B.S.; Eamon, C.T.; Johnson, A.E.
J. Biol. Chem. 260, 2583, 1985
A;Reference number: A37544
A;Contents: annotation; calcium binding, correction
R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
Cell 45, 343-348, 1986
A;Title: Defective propeptide processing of blood clotting factor IX caused by mutation c
A;Reference number: A37545; MUID:86189947; PMID:3009023
A;Contents: annotation; signal sequence cleavage site
R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
J. Biol. Chem. 264, 21257-21265, 1989
A;Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
A;Reference number: A30622; MUID:90078229; PMID:2592373
A;Contents: annotation; sequence of mutant B(M) Nagoya
A;Note: carboxylation, glycosylation, and cleavage sites
R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee
submitted to the Brookhaven Protein Data Bank, November 1991
A;Reference number: A51252; PDB:1IXA
A;Contents: annotation; conformation by (1)H-NMR, residues 92-130
A;Note: recombinant form expressed in yeast
C;Comment: Factor IX is activated by factor XIa, which excises the activation peptide pro
C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stror
C;Genetics:
A;Gene: GDB:F9
A;Cross-references: GDB:119900; OMIM:306900
A;Map position: Xq27.1-Xq27.2
A;Introns: 30/1; 84/2; 93/1; 174/1; 241/3; 280/1
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor X in the preser
A;Pathway: blood coagulation intrinsic pathway
C;Keywords: coagulation factor X; EGF homology; Gla domain homology; trypsin homology.
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-46/Domain: propeptide #status experimental <PPT>
F;31-91/Domain: Gla domain homology <GLA>
F;47-131/Product: coagulation factor IXa light chain #status experimental <ALC>
F;97-128/Domain: EGF homology <EG1>
F;134-170/Domain: EGF homology <EG2>
F;192-226/Domain: activation peptide #status experimental <ACT>

A;Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali
A;Reference number: A12453; MUID:73053314; PMID:4284286
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to f
A;Reference number: A13504; MUID:76053121; PMID:11059122
A;Contents: annotation; activation
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of tw
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), o
activation.
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Gene: F10
A;Map position: 13q34
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-180/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG>
F;129-164/Domain: EGF homology <EG2>
F;183-493/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-493/Domain: activation peptide #status experimental <APT>
F;234-492/Product: coagulation factor Xa heavy chain #status experimental <ANC>
F;234-461/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #st
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status pi
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
P;200/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental
F;208,485/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;233-234/Cleavage site: Arg-Ile (coagulation factor Ixa, coagulation factor VIIa) #statu
F;240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
F;275,321,418/Active site: His, Asp, Ser #status predicted

Query Match 45.7%; Score 90.5; DB 1; Length 492;
Best Local Similarity 42.2%; Pred.No.3.le-07;
Matches 19; Conservative 7; Mismatches 18; Indels 1; Gaps 1;

QY 1 ANAGFLXXLRPGSLRXKXQCFFXARXIFKDAXRTKLFWISY 45
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
db 41 ANS-FLEEVKGNGLERCLEACSLBEAREVFEDAEQTDFWSKY 84
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 12
S18994
protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A;Description: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994
A;Accession: S18994
A;Status: preliminary
A;Molecule type: mRNA

Search completed: August 22, 2005, 18:46:44
Job time : 26 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 83 Seconds
(without alignments)
277.633 Million cell updates/sec

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANAGFLXLRGSLRXCKX.....XXARXIFKDXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	161.5	81.6	466	1	FA7_HUMAN	P08709 homo sapien
2	161.5	81.6	679	2	Q96PQ8	Q96PQ8 homo sapien
3	127.5	64.4	444	1	FA7_RABIT	P98139 oryctolagus
4	119	60.1	407	1	FA7_BOVIN	P22457 bos taurus
5	118	59.6	443	2	Q8JHC9	Q8JHC9 brachydanio
6	116.5	58.8	446	1	FA7_MOUSE	P70375 mus musculus
7	103.5	52.3	459	1	PRTC_PIG	Q9GLP2 sus scrofa
8	103	52.0	442	2	Q804X1	Q804X1 fugu rubrip
9	101	51.0	537	2	Q804W8	Q804W8 fugu rubrip
10	98.5	49.7	460	1	PRTC_MOUSE	P33587 mus musculus
11	95	48.0	218	1	TWGI_HUMAN	O14668 homo sapien
12	95	48.0	266	2	Q8NEK6	Q8NEK6 homo sapien
13	95	48.0	617	1	THRB_RAT	P18292 rattus norv
14	95	48.0	618	1	THRB_MOUSE	P19221 mus musculus
15	93.5	47.2	446	1	FA7_RAT	Q8K3U6 rattus norv
16	93.5	47.2	456	1	PRTC_BOVIN	P00745 bos taurus
17	93	47.0	49	2	Q9SME8	Q9SME8 bos taurus
18	93	47.0	416	1	FA9_BOVIN	P00741 bos taurus
19	92.5	46.7	462	2	Q6PAG2	Q6PAG2 xenopus lae
20	92	46.5	179	2	Q8TAS3	Q8TAS3 homo sapien
21	92	46.5	198	1	TWGI_MOUSE	Q8182 mus musculus
22	92	46.5	202	1	TWGI_HUMAN	O14669 homo sapien
23	91.5	46.2	488	1	FA10_HUMAN	P00742 homo sapien
24	91	46.0	433	2	Q8JHD0	Q8JHD0 brachydanio
25	91	46.0	433	2	Q90YK1	Q90YK1 brachydanio
26	91	46.0	461	1	FA9_HUMAN	P00740 homo sapien
27	91	46.0	461	1	FA9_PANTR	Q95ND7 pan troglod
28	91	46.0	461	2	Q95ND6	Q95ND6 pan troglod
29	90.5	45.7	425	2	Q804X7	Q804X7 gallus gall
30	90.5	45.7	492	1	FA10_BOVIN	P00743 bos taurus
31	90	45.5	471	2	Q804X6	Q804X6 gallus gall

32	89.5	45.2	461	1	PRTC_RAT	P11394 rattus norv
33	89.5	45.2	461	2	Q88FY8	Q88FY8 rattus norv
34	89	44.9	216	2	Q6DIH4	Q6DIH4 xenopus tro
35	88.5	44.7	433	2	Q804X5	Q804X5 gallus gall
36	88	44.4	466	2	Q6SA95	Q6SA95 felis silve
37	87.5	44.2	490	1	FA10_RABIT	O19045 oryctolagus
38	86	43.4	208	2	Q6GPL7	Q6GPL7 xenopus lae
39	86	43.4	376	1	FA10_TROCA	P81428 tropidechis
40	85.5	43.2	469	2	Q9GMD9	Q9GMD9 ornithorhyn
41	85.5	43.2	482	1	FA10_RAT	Q63207 rattus norv
42	85	42.9	434	2	Q7T3B6	Q7T3B6 brachydanio
43	85	42.9	452	1	FA9_CANFA	P19540 canis famil
44	85	42.9	459	1	FA9_MOUSE	P16294 mus musculu
45	84	42.4	376	1	FA10_HOPST	P83370 hoplocephal

ALIGNMENTS

RESULT 1
ID - FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (SPCA) (Proconvartin) (Eptacog alfa).
GN Name=F7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.B., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.B., Inley M.Y., Kiesel W., Kurachi K.,
RA Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Inley M.Y.,
RA Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi O., Nickerson D.A.;
RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=9088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kiesel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine.";

RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor VIIa
RT with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
RA Zhang E., St. Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPRI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.S., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human
RT factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patraccchini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Caonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7)." ;
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patraccchini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms
RT (115His and 333Ser) in the human coagulation factor VII gene." ;
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of

RT coagulation factor VII." ;
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94264305; PubMed=8204879;
RA Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the
RT cleavage site for activation and altering binding to tissue factor." ;
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT SER-367.
RX PubMed=7860081;
RA Dewald G., Noethen M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of
RT human complement component C7." ;
RL Hum. Hered. 44:301-304(1994).
RN [17]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala-->Sval) and X (334Ser-->Pro)." ;
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [18]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayaashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
RT catalytic domain." ;
RL Thromb. Haemost. 71:773-777(1994).
RN [19]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule." ;
RL Blood 87:5085-5094(1996).
RN [20]
RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU2>3.3.CO;2-6;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII
RT deficiency." ;
RL Hum. Mutat. 8:108-115(1996).
RN [21]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
RA Seligsohn U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews." ;
RL Thromb. Haemost. 76:283-291(1996).
RN [22]
RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
RT the signal sequence identified in a patient with factor VII
RT deficiency." ;
RL Br. J. Haematol. 101:47-49(1998).
RN [23]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alehinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation
RT factor VII gene." ;

Query Match 81.6%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 1.6e-19;
Mismatches 0; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAGFLXXLRPGSLRXKXQCSPFXARXIFKDARTKLFWISY 45
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DB 61 ANA-FLEELRPGSLEKECKEQSPPEARIFPKDAERTKLFWISY 104

RESULT 2

ID Q96PQB PRELIMINARY; PRT; 679 AA.

AC Q96POB; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
Hu Z., Garen A.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF272774; AAK58686.2; -.
DR HSSP; P08709; IGLI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPRO00152; Asx hydroxyl_S.
DR InterPro; IPRO00742; EGF_2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03597; Ig cl.
DR InterPro; IPRO03006; IG_MHC.
DR InterPro; IPRO01254; Peptide S1.
DR InterPro; IPRO09003; Pept Ser_Cys.
DR InterPro; IPRO00294; Vitk_dep_GLA.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGLI; 1.
DR PROSITE; PS00020; Tryp spc; 1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 679 AA; 75552 MW; OB0023AE70A057AI CRC64;

Hum. Mutat. Suppl. 1:S189-S191(1998).

Query Match 81.6%; Score 161.5; DB 2; Length 679;
Best Local Similarity 75.6%; Pred. No. 2.3e-19;
Mismatches 0; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAGFLXXLRPGSLRXKXQCSPFXARXIFKDARTKLFWISY 45
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 ANA-FLEELRPGSLEKECKEQSCFEAREIFKDAERTKLFWISY 82

RESULT 3

PA7_RABIT STANDARD; PRT; 444 AA.

AC P98139; P79224; DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN Name=F7;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctologus.
NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=93190306; PubMed=8383365; DOI=10.1016/0049-3848(93)90048-S;
Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RL Thromb. Res. Suppl. 69:231-238(1993).
RN [2]
REVISION TO 395.
RP TISSUE=Liver;
RC Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL FunctioN: Initiates the extrinsic pathway of blood coagulation.
CC Serine protease that circulates in the blood in a zymogen form.
CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa,
CC factor IXa, or thrombin by minor proteolytic cleavages. In the presence of
CC tissue factor and calcium ions, factor VIIa then converts factor X
CC to factor IXa by limited proteolysis. Factor VIIa will also convert
CC factor IX to factor IXa in the presence of tissue factor and
CC calcium (By similarity).
CC CATALYTIC ACTIVITY: Hydrolyzes one Arg--|-ile bond in factor X to
CC form factor Xa.
CC SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond (By similarity).
CC TISSUE SPECIFICITY: Plasma.
CC PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium (By
CC similarity).
CC SIMILARITY: Belongs to the peptidase S1 family.
CC SIMILARITY: Contains 2 EGF-like domains.
CC SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
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EMBL; U77477; AAB37326.1; -.
HSSP; P08709; IFAP.
MEROPS; S01.215; -.
InterPro; IPRO00152; Asx hydroxyl_S.
InterPro; IPRO00742; EGF_2.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO01438; EGF II.

RESULT 5	Q8JHC9	PRELIMINARY;	PRT;	443 AA.
ID	Q8JHC9			
AC	Q8JHC9;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Coagulation factor VIII.			
GN	Namesf1;			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hanumanthaiah R.; Day K.; Jagadeeswaran P.;			
RT	"Comprehensive analysis of blood coagulation pathways in Teleostei;			
RT	Evolution of coagulation factor genes and identification of zebrafish			
RT	factor VIII.";			
RC	Blood Cells Mol. Dis. 0:0-0(2002).			
CC	-1- SIMILARITY: Belongs to peptidase family S1.			
CC	-1- SIMILARITY: Contains 1 EGF-like domain.			
DR	EMBL; AF519546; AAM88342.1; -			
DR	EMBL; AF515269; AAN71000.1; -			
DR	HSSP; P00740; 1CFH.			
DR	ZFIN; ZDB-GENE-021206-10; f71.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR	GO; GO:0008233; F:peptidase activity; IEA.			
DR	GO; GO:0004295; F:trypsin activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000742; EGF 2.			
DR	InterPro; IPR006209; EGF-like.			
DR	InterPro; IPR002383; GLA_blood.			
DR	InterPro; IPR062210; IEGF.			
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR001314; Peptidase_S1A.			
DR	InterPro; IPR009003; Pept_Ser_Cys.			
DR	InterPro; IPR000294; VitK_dep_GLA.			
DR	Pfam; PF00008; EGF; 1.			
DR	Pfam; PF00594; Gla; 1.			
DR	Pfam; PF00089; Trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PRINTS; PR00001; GLABLOOD.			
DR	SMART; SM00181; EGF; 2.			
DR	SMART; SM00069; GLA; 1.			
DR	SMART; SM00020; Tryp_Spc; 1.			
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE; PS01186; EGF_2; 2.			
DR	PROSITE; PS50026; EGF_3; 1.			
DR	PROSITE; PS00011; GLA_1; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.			
KW	EGF-like domain; Hydrolase; Protease; Serine protease.			
SQ	SSSEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;			
Query Match	59.6%;	Score 118;	DB 2;	Length 443;
Best Local Similarity	46.7%;	Pred. No. 6.8e-12;		
Matches 21; Conservative	8;	Mismatches 16;	Indels 0;	Gaps
Qy	1	ANAGFLXLRPGLSRXKXKXQCSFXAXRIFPKDAXRTKLFWISY 45		
Db	38	ANGSFLFEEMKAGNRECVETICDYEEAREVEDDDRTKQFWLSY 82		

[illegible]

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
 DE conversion accelerator).
 GN Name=F7; Synonyms=Cf7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96276538; PubMed=8701412;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RA Castellino F.J.;
 RA "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97127167; PubMed=8972017;
 RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
 RA "Nucleotide structure and characterization of the murine blood
 RT coagulation factor VII gene.";
 RL Thromb. Haemost. 76:957-964(1996).
 CC -1- FUNCTION: Initiates the extrinsic pathway of blood coagulation.
 CC Serine protease that circulates in the blood in a zymogen form.
 CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa,
 CC factor IXa, or thrombin by minor proteolysis. In the presence of
 CC tissue factor and calcium ions, factor VIIa then converts factor X
 CC to factor Xa by limited proteolysis. Factor VIIa will also convert
 CC factor IX to factor IXa in the presence of tissue factor and
 CC calcium (By similarity).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 CC a disulfide bond (By similarity).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some
 CC glutamate residues allows the modified protein to bind calcium (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC ENBL; U44795; AAC52570.1; -;
 CC EMBL; U66079; AAC33796.1; -;
 CC HSP; P08709; 1BF9.
 CC MEROPS; S01.215; -;
 CC MGD; MGI:109325; F7.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001438; EGF_II.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR002383; Gla_blood.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1.
 CC InterPro; IPR009003; Peptidase_S1A.
 CC InterPro; IPR000294; VitK_dep_Gla.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; Gla; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00010; EGFBL00.
 CC PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 41 Potential.
 FT CHAIN 42 193 Factor VII light chain.
 FT CHAIN 194 446 Factor VII heavy chain.
 FT DOMAIN 42 86 Gla.
 FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 128 169 EGF-like 2.
 FT DOMAIN 194 446 Serine protease.
 FT SITE 193 194 Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin) (By similarity).
 FT ACT_SITE 234 234 By similarity.
 FT ACT_SITE 283 283 By similarity.
 FT ACT_SITE 385 385 By similarity.
 FT BINDING 379 379 Substrate (By similarity).
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 102 By similarity.
 FT DISULFID 96 111 By similarity.
 FT DISULFID 113 122 By similarity.
 FT DISULFID 132 143 By similarity.
 FT DISULFID 139 153 By similarity.
 FT DISULFID 155 168 By similarity.
 FT DISULFID 176 303 By similarity.
 FT DISULFID 200 205 By similarity.
 FT DISULFID 219 235 By similarity.
 FT DISULFID 351 370 By similarity.
 FT DISULFID 381 409 By similarity.
 FT MOD_RES 47 47 4-carboxyglutamate.
 FT MOD_RES 48 48 4-carboxyglutamate.
 FT MOD_RES 55 55 4-carboxyglutamate.
 FT MOD_RES 57 57 4-carboxyglutamate.
 FT MOD_RES 60 60 4-carboxyglutamate.
 FT MOD_RES 61 61 4-carboxyglutamate.
 FT MOD_RES 66 66 4-carboxyglutamate.
 FT MOD_RES 67 67 4-carboxyglutamate.
 FT MOD_RES 70 70 4-carboxyglutamate.
 FT MOD_RES 76 76 4-carboxyglutamate.
 FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
 FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 99 99 G -> V (in Ref. 2).
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45CBC96E CRC64;
 Query Match 58.8%; Score 116.5; DB 1; Length 446;
 Best Local Similarity 57.8%; Pred. NO. 1.9e-11;
 Matches 26; Conservative 1; Mismatches 17; Indels 1; Gaps 1;
 QY 1 ANAGFLXLRPGSLRXKXQCSPXXARXIFKDXRTKLFWSY 45
 DB 42 ANS-LLEELWPGSLERECEEQSPFEAREIFKSPERTKQFWIV 85
 RESULT 7
 ID_PRTC_PIG STANDARD; PRT; 459 AA.
 AC O9GLE2; AC
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
 DE Name=PROC;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J., Kim H.K.W.;
 RA "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains";
 RT Cell. Mol. Life Sci. 58:148-159(2001).
 RL
 CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (GLA) domain.
 CC
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 CC
 DR EMBL; AF191307; AAG28380.1; -.
 DR HSSP; P04070; 1AUT.
 DR MEROPS: S01.218; -.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR00294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_SER; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 41 By similarity.
 FT CHAIN 42 459 Vitamin K-dependent protein C.
 FT CHAIN 42 196 Vitamin K-dependent protein C light chain (By similarity).
 FT CHAIN 199 459 Vitamin K-dependent protein C heavy chain (By similarity).
 FT PEPTIDE 199 213 Activation peptide (By similarity).
 FT SITE 213 214 Cleavage (by thrombin) (By similarity).
 FT DOMAIN 42 87 Gla.
 FT DOMAIN 96 131 EGF-like 1.
 FT DOMAIN 135 175 EGF-like 2.
 FT DOMAIN 214 459 Serine protease.
 FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
 FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE 255 255 Charge relay system.
 FT ACT_SITE 301 301 Charge relay system.
 FT ACT_SITE 400 400 Charge relay system.
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 110 By similarity.
 FT DISULFID 100 105 By similarity.
 FT DISULFID 104 119 By similarity.
 FT DISULFID 121 130 By similarity.
 FT DISULFID 139 150 By similarity.
 FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 321 Interchain (By similarity).
 FT DISULFID 240 256 By similarity.
 FT DISULFID 371 385 By similarity.
 FT DISULFID 396 424 By similarity.
 FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;

Query Match 52.3%; Score 103.5; DB 1; Length 459;
 Best Local Similarity 48.9%; Pred. No. 2.5e-09;
 Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

Oy 1 ANAGFLXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWSY 45

Db 42 ANS-FLSELPSLSRECKGETCDFEAREIFQNTENTMAFWSKY 85

RESULT 8

ID Q804X1 PRELIMINARY; PRT; 442 AA.

AC Q804X1; 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Coagulation factor VIIb (EC 3.4.21.21).

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 DR EMBL; AF465274; AAO33369.1; -.
 DR HSSP; P00740; 1CGF.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004283; F:chymotrypsin activity; IEA.
 DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR009003; Pept Ser Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00089; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 442 AA; 48787 MW; 810A561A127F0CE7 CRC64;
 Query Match 52.0%; Score 103; DB 2; Length 442;
 Best Local Similarity 40.0%; Pred. No. 3e-09;
 Matches 18; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
 Qy 1 ANAGFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 38 ANSGFLEMQGNLKRCIEICNYEARVEFDQAQTRKFWET 82
 RESULT 9
 Q804W8 PRELIMINARY; PRT; 537 AA.
 ID Q804W8;
 AC Q804W8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Coagulation factor IX (EC 3.4.21.22).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; AF465277; AAO33372.1; -.
 DR HSSP; P00760; 1EZK.
 DR MEROPS; S01.215; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003803; F:coagulation factor IXa activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR009003; Pept Ser Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR PRINTS; PR00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 537 AA; 60449 MW; ABD40ADPB7F23851 CRC64;
 Query Match 51.0%; Score 101; DB 2; Length 537;
 Best Local Similarity 40.9%; Pred. No. 8.1e-09;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 Qy 2 NAGFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 47 NSGHLLELQKDLNLERCKEEOCTMEAEARVEFDEKTAERFWGY 90
 RESULT 10
 PRTC MOUSE STANDARD; PRT; 460 AA.
 ID PRTC MOUSE
 AC P33587; O35498; Q91WN8; Q99PC6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolysis of protein C) (Anticoagulant protein C) (Blood coagulation factor XIV).
 DE Name=Proc;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;

RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C";
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Korf I.;
RT "Complete sequence of UC72A01";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 274-433 FROM N.A.
RC STRAIN=BALB/C;
RA MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C";
RL Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC
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or send an email to license@isb-sib.ch.
CC -----
CC EMBL; D10445; BAA01235.1; --
DR EMBL; AF034569; AAC33795.1; --
DR EMBL; AF318182; AAK07918.1; --
DR EMBL; BC013896; AAHL3896.1; --
DR EMBL; D43755; BAA07812.1; --
DR PIR; JX0210; JX0210.
DR HSSP; P04070; LAUT.
DR MEROPS; S01.218; --
DR MGD; MGI:97771; PROC.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
Repeat; Serine protease; Signal; Vitamin K.
FT SIGNAL; 1 33 By similarity.
FT PROPEP; 34 41 Vitamin K-dependent protein C.
FT CHAIN; 42 460 Vitamin K-dependent protein C light chain
FT CHAIN; 42 196 (By similarity).
FT CHAIN; 199 460 Vitamin K-dependent protein C heavy chain
FT CHAIN; 199 460 (By similarity).
FT PEPTIDE; 199 212 Activation peptide (By similarity).
FT SITE; 212 213 Cleavage (by thrombin) (By similarity).
FT DOMAIN; 42 87 Gla.
FT DOMAIN; 96 131 EGF-like 1.
FT DOMAIN; 135 175 EGF-like 2.
FT DOMAIN; 213 460 Serine protease.
FT MOD_RES; 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES; 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES; 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES; 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES; 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES; 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES; 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES; 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES; 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES; 112 112 3-hydroxyaspartate (By similarity).
FT ACT_SITE; 253 253 Charge relay system.
FT ACT_SITE; 299 299 Charge relay system.
FT ACT_SITE; 401 401 Charge relay system.
FT DISULFID; 58 63 By similarity.
FT DISULFID; 91 110 By similarity.
FT DISULFID; 100 105 By similarity.
FT DISULFID; 104 119 By similarity.
FT DISULFID; 121 130 By similarity.
FT DISULFID; 139 150 By similarity.

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FT DISULFID 146 159 By similarity.
FT FT 161 174 By similarity.
FT DISULFID 182 319 Interchain (By similarity).
FT DISULFID 238 254 By similarity.
FT DISULFID 372 386 By similarity.
FT DISULFID 397 425 By similarity.
FT CARBOHYD 214 214 N-linked (GlcNAc...) (potential).
FT CARBOHYD 290 290 N-linked (GlcNAc...) (potential).
FT CARBOHYD 354 354 N-linked (GlcNAc...) (potential).
FT VARIANT 327 327 Q -> QQ (in strain BALB/c).
FT VARIANT 392 392 D -> N (in strain BALB/c).
FT CONFLICT 65 65 F -> L (in Ref. 3).
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E86FC274 CRC64;

Query Match 49.7%; Score 98.5; DB 1; Length 460;
Best Local Similarity 46.7%; Pred. No. 1.9e-06;
Matches 21; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCXFXRXRXIFKDXRTKLFWSY 45
Db 42 ANS-FLEEMRPGSLRECMIEICDFE8AQBIQFQNVDTLAFWKY 85

RESULT 11
TMG1 HUMAN
ID TMG1_HUMAN STANDARD; PRT; 218 AA.
AC O14658;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-rich
DE rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
DE 1).
GN Name=PRG1; Synonyms=PRGP1, TMG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434; DOI=10.1073/pnas.94.17.9058;
RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC pro- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -!- PWM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamate by a vitamin K-dependent gamma-
CC carboxylase.

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CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF009242; AA67070.1; -.
CC EMBL; BC060833; AA670833.1; -.
CC HSP; P00740; ICFH.
CC Genew; HGNC:9469; PRRG1.
CC MM; 604428; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00594; Gla; 1.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00069; GLA; 1.
CC PROSITE; PS00011; GLA_1; 1.
CC PROSITE; PS00998; GLA_2; 1.
CC KW Gamma-carboxyglutamic acid; Transmembrane; Vitamin K.
FT PROPEP 1 20
FT CHAIN 21 218 Transmembrane gamma-carboxyglutamic acid
FT protein 1.
FT DOMAIN 21 83 Extracellular (Potential).
FT TRANSMEM 84 106 Potential.
FT DOMAIN 107 218 Cytoplasmic (Potential).
FT DOMAIN 21 66 Gla.
FT DOMAIN 131 135 Poly-Pro.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;

Query Match 48.0%; Score 95; DB 1; Length 218;
Best Local Similarity 40.5%; Pred. No. 3.8e-08;
Matches 17; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 4 GFLXLRPGSLRXCKXXQCXFXRXRXIFKDXRTKLFWSY 45
Db 23 GPFPIRQGNIERECKEECTFEAREAFENNEKTFEWSY 64

RESULT 12
Q8NEK6
ID Q8NEK6 PRELIMINARY; PRT; 266 AA.
AC Q8NEK6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PRRG1 protein (Fragment).
GN Names=PRRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030786; AH30786.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLA 1; 1.
FT NON TER
FT 1
SQ SEQUENCE 266 AA; 30151 MW; 175768D24D635351 CRC64;

Query Match 48.0%; Score 95; DB 2; Length 266;
Best Local Similarity 40.5%; Pred. No. 4.6e-08;
Matches 17; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 GFLXXLRGSLRXCKXQCFSXXARXIFKDXRXTKLFWISY 45
DB 71 GFEEIROGNIREECKEFCTFEAREAPENNEKTFWSTY 112

RESULT 13
THRB_RAT
ID THRB_RAT STANDARD; PRT; 617 AA.
AC P18292;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN Name=P2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=90332426; PubMed=2377469;
RA Dihanich M., Monard D.;
RT "cDNA sequence of rat prothrombin.";
RL Nucleic Acids Res. 18:4251-4251(1990).
RN [2]
RP SEQUENCE OF 383-617 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., McGillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- PTM: The gamma-carboxyglutamyl residues, which bind calcium ions,
CC result from the carboxylation of glutamyl residues by a microsomal
CC enzyme, the vitamin K-dependent carboxylase. The modified residues
CC are necessary for the calcium-dependent interaction with a

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CC negatively charged phospholipid surface, which is essential for
CC the conversion of prothrombin to thrombin.
CC -1- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -1- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -1- SIMILARITY: Belongs to the peptidase S1 family.
CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -1- SIMILARITY: Contains 2 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; X52835; CAA37017.1; -.
DR EMBL; M81397; AAA42240.1; -.
DR PIR; S10511; S10511.
DR HSSP; P00734; 1UUVS.
DR MEROPS; S01-217; -.
DR RGD; 61996; P2.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS50070; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_HIS; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Acute phase; Blood coagulation; Calcium-binding;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Kringle; Plasma;
KW Repeat; Serine protease; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 43
FT CHAIN 44 617 Prothrombin.
FT PEPTIDE 44 200 Activation peptide (fragment 1).
FT PEPTIDE 201 323 Activation peptide (fragment 2).
FT CHAIN 324 359 Thrombin light chain.
FT CHAIN 360 617 Thrombin heavy chain.
FT DOMAIN 44 90 Gla.
FT DOMAIN 109 187 Kringle 1.
FT DOMAIN 215 292 Kringle 2.
FT DOMAIN 360 617 Serine protease.
FT SITE 200 201 Cleavage (by thrombin).
FT SITE 323 324 Cleavage (by factor Xa).
FT SITE 359 360 Cleavage (by factor Xa).

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FT ACT SITE 402 Charge relay system (By similarity).
FT ACT SITE 458 Charge relay system (By similarity).
FT ACT SITE 564 Charge relay system (By similarity).
FT MOD_RES 50 4-carboxyglutamate.
FT MOD_RES 51 4-carboxyglutamate.
FT MOD_RES 58 4-carboxyglutamate.
FT MOD_RES 60 4-carboxyglutamate.
FT MOD_RES 63 4-carboxyglutamate.
FT MOD_RES 64 4-carboxyglutamate.
FT MOD_RES 69 4-carboxyglutamate.
FT MOD_RES 70 4-carboxyglutamate.
FT MOD_RES 73 4-carboxyglutamate.
FT MOD_RES 76 4-carboxyglutamate.
FT CARBOHYD 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 412 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 552 N-linked (GlcNAc...) (Potential).
FT DISULFID 61 By similarity.
FT DISULFID 91 By similarity.
FT DISULFID 109 By similarity.
FT DISULFID 130 By similarity.
FT DISULFID 158 By similarity.
FT DISULFID 215 By similarity.
FT DISULFID 236 By similarity.
FT DISULFID 264 By similarity.
FT DISULFID 332 Interchain (By similarity).
FT DISULFID 387 By similarity.
FT DISULFID 532 By similarity.
FT DISULFID 560 By similarity.
SQ SEQUENCE 617 AA; 70411 MW; AD27D1B71445DB1D CRC64;

Query Match 48.0%; Score 95; DB 1; Length 617;
Best Local Similarity 42.2%; Pred. No. 1.1e-07;
Matches 19; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ANAGFLXXLRGSLRXKXXQCSFXXARIFKDXRTKLFWSY 45
Db 44 ANSGFLBRLKGNLRECBQCSYEFALFSALESPQDITVFWAKY 88

RESULT 14
THRB MOUSE STANDARD; PRT; 618 AA.
AC P19221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN Name=F2; Synonyms=Cf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025551; PubMed=2222810;
RA Friezner Degen S.J.; Schaffer L.A.; Jamison C.S.; Grant S.G.;
RA Fitzgibbon J.J.; Pai J.-A.; Chapman V.M.; Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RL localization of the gene on mouse chromosome 2.";
RN DNA Cell Biol. 9:487-498(1990).
[2]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=2388257; PubMed=242603899;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haieh F.;
RA Diatchenko L.; Narusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
SEQUENCE OF 384-618 FROM N.A.
TISSUE=Liver;
MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.;
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
CC -I- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VIII, XIII,
CC XII, and, in complex with thrombomodulin, protein C.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-[Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -I- PTM: The gamma-carboxyglutamyl residues, which bind calcium ions,
CC result from the carboxylation of glutamyl residues by a microsomal
CC enzyme, the vitamin K-dependent carboxylase. The modified residues
CC are necessary for the calcium-dependent interaction with a
CC negatively charged phospholipid surface, which is essential for
CC the conversion of prothrombin to thrombin.
CC -I- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -I- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -I- SIMILARITY: Belongs to the peptidase S1 family.
CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -I- SIMILARITY: Contains 2 kringle domains.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52308; CAA36548.1; -.
CC EMBL; BC013662; AAH13662.1; -.
CC EMBL; M81394; AAA0435.1; -.
CC FIR; A35827; A35827.
CC HSSP; P00734; 1B7X.
CC MEROPS; S01.217; -.
CC MGD; MGI:88380; F2.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR003966; Peptidase_S1A_pr.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00594; Gla; 1.
CC Pfam; PF00051; Kringle; 2.
CC Pfam; PF00089; Trypsin; 1.

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DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Calcium-binding; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 Potential.
FT PROPEP 25 41 Potential.
FT CHAIN 42 193 Factor VII light chain (By similarity).
FT CHAIN 194 446 Factor VII heavy chain (By similarity).
FT DOMAIN 42 86 Gla.
FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 128 169 EGF-like 2.
FT DOMAIN 194 446 Serine protease.
FT SITE 193 194 Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin) (By similarity).
FT ACT_SITE 234 234 By similarity.
FT ACT_SITE 283 283 By similarity.
FT ACT_SITE 385 385 By similarity.
FT BINDING 379 379 Substrate (By similarity).
FT DISULFID 58 63 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 96 111 By similarity.
FT DISULFID 113 122 By similarity.
FT DISULFID 132 143 By similarity.
FT DISULFID 139 153 By similarity.
FT DISULFID 155 168 By similarity.
FT DISULFID 176 303 By similarity.
FT DISULFID 200 205 By similarity.
FT DISULFID 219 235 By similarity.
FT DISULFID 351 370 By similarity.
FT DISULFID 381 409 By similarity.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 76 76 4-carboxyglutamate (By similarity).
FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 446 AA; 50399 MW; 292985EBF119C0AA CRC64;

Query Match 47.2%; Score 93.5; DB 1; Length 446;
Best Local Similarity 48.9%; Pred. No. 1.4e-07;
Matches 22; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXKXXQCXFXXARXIFKDXFTKLFWSY 45
| | | | | : | | | | | | | | | | | | | | | |
Db 42 ANS-LLEELWSSSLERECEERCSFEARIFKSPERTKQFTIY 85

Search completed: August 22, 2005, 18:42:26
Job time : 84 secs

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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:42:23 ; Search time 30 Seconds
(without alignments)
111.974 Million cell updates/sec

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANAGFLXXLRPGSLRXCKX.....XXARXIFKDXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.6	44	3	US-08-955-636-3
2	161.5	81.6	44	4	US-09-302-239-3
3	161.5	81.6	44	4	US-09-497-591-3
4	161.5	81.6	44	4	US-09-803-810-3
5	161.5	81.6	406	1	US-08-293-778-24
6	161.5	81.6	406	1	US-08-295-411-5
7	161.5	81.6	406	2	US-08-955-471-5
8	161.5	81.6	406	4	US-09-782-587B-1
9	161.5	81.6	406	4	US-09-782-587B-3
10	161.5	81.6	406	5	PCT-US92-10242-5
11	161.5	81.6	444	1	US-08-475-845-2
12	161.5	81.6	444	2	US-08-327-690-2
13	161.5	81.6	444	2	US-08-660-289-2
14	161.5	81.6	444	2	US-08-537-807-2
15	161.5	81.6	444	2	US-08-871-003-2
16	161.5	81.6	444	3	US-08-464-233-2
17	161.5	81.6	444	3	US-09-189-607-2
18	161.5	81.6	444	3	US-09-378-907-2
19	161.5	81.6	444	5	PCT-US94-05779-2
20	161.5	81.6	461	4	US-09-949-016-8839
21	161.5	81.6	466	1	US-07-882-202A-4
22	161.5	81.6	466	1	US-08-021-615A-4
23	161.5	81.6	466	1	US-08-321-777-4
24	161.5	81.6	466	3	US-09-009-217-14
25	161.5	81.6	466	3	US-09-009-656-14
26	161.5	81.6	466	5	PCT-US93-04493-4
27	161.5	81.6	483	4	US-09-949-016-9523

28	155.5	78.5	44	3	US-08-955-636-29	Sequence 29, Appl
29	153.5	77.5	44	3	US-08-955-636-26	Sequence 26, Appl
30	153.5	77.5	44	3	US-08-955-636-27	Sequence 27, Appl
31	153.5	77.5	44	3	US-08-955-636-28	Sequence 28, Appl
32	149.5	75.5	44	3	US-08-955-636-30	Sequence 30, Appl
33	146.5	74.0	41	1	US-08-229-280-4	Sequence 4, Appl
34	142.5	72.0	42	4	US-09-383-667-7	Sequence 7, Appl
35	127	64.1	44	3	US-08-955-636-4	Sequence 4, Appl
36	127	64.1	44	4	US-09-302-239-4	Sequence 4, Appl
37	127	64.1	44	4	US-09-497-591-4	Sequence 4, Appl
38	127	64.1	44	4	US-09-803-810-4	Sequence 4, Appl
39	100.5	50.8	139	1	US-08-330-978-2	Sequence 2, Appl
40	100.5	50.8	139	1	US-08-474-042-2	Sequence 2, Appl
41	100.5	50.8	139	1	US-08-484-558-2	Sequence 2, Appl
42	100.5	50.8	139	1	US-08-774-592-2	Sequence 2, Appl
43	100.5	50.8	437	1	US-08-487-037-2	Sequence 2, Appl
44	100.5	50.8	437	1	US-08-487-037-3	Sequence 3, Appl
45	100.5	50.8	488	1	US-08-487-037-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955.636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3

Query Match	81.6%	Score 161.5;	DB 3;	Length 44;
Best Local Similarity	97.8%	Pred. No. 5.8e-20;		
Matches	44;	Conservative	0;	Mismatches
			0;	Indels
				1;
				Gaps
				1;

Qy	1	ANAGFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 45
Db	1	ANA-FLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 2
US-09-302-239-3
; Sequence 3, Application US/09302239
; Patent No. 6693075
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/302,239
; CURRENT FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 3
US-09-497-591-3
; Sequence 3, Application US/09497591
; Patent No. 6747003
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; CURRENT FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 4
US-09-803-810-3
; Sequence 3, Application US/09803810
; Patent No. 6762286
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 5.8e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

Query Match 81.6%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXLRPGSLXRCXKXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLYLRPGSLRYCKYQCSFYARYIFKDXRTKLFWISY 44

RESULT 6
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/1994
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5
Query Match 81.6%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLRXCKXQCSPFXARXIFKDXRKLFWISY 45
Db 1 ANA-FLESLRPGSLRECKEKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5
Query Match 81.6%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLRXCKXQCSPFXARXIFKDXRKLFWISY 45
Db 1 ANA-FLESLRPGSLRECKEKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26

; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5
Query Match 81.6%; Score 161.5; DB 2; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ANAGFLXXLRPGSLRXCKXQCSPFXARXIFKDXRKLFWISY 45
Db 1 ANA-FLESLRPGSLRECKEKEQCSFEAREIFKDAERTKLFWISY 44
RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26

Query Match 81.6%; Score 161.5; DB 4; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;

RESULT 11
US-08-475-845-2

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; Sequence 2, Application US/08475845
; Patent No. 5788965
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,845
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,690
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-845-2

Query Match 81.6%; Score 161.5; DB 1; Length 444;
Best Local Similarity 75.6%; Pred. No. 6.3e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXIFKDAKTKLFWISY 45
Db 39 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-327-690-2
; Sequence 2, Application US/08327690
; Patent No. 5817788
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
```

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; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,690
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/065,725
; FILING DATE: 21-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-327-690-2

Query Match 81.6%; Score 161.5; DB 2; Length 444;
Best Local Similarity 75.6%; Pred. No. 6.3e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXIFKDAKTKLFWISY 45
Db 39 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5833982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	161.5	81.6	44	9	US-09-803-810-3	Sequence 3
2	161.5	81.6	44	14	US-10-298-330-3	Sequence 1
3	161.5	81.6	44	16	US-10-855-068-3	Sequence 1
4	161.5	81.6	406	10	US-09-782-587B-1	Sequence 1
5	161.5	81.6	406	10	US-09-782-587B-3	Sequence 1
6	161.5	81.6	406	14	US-10-109-498-1	Sequence 1
7	161.5	81.6	406	14	US-10-255-032-1	Sequence 1
8	161.5	81.6	406	14	US-10-281-727-1	Sequence 1
9	161.5	81.6	406	15	US-10-386-898-7	Sequence 1
10	161.5	81.6	406	15	US-10-383-898-1	Sequence 1
11	161.5	81.6	406	15	US-10-617-500-1	Sequence 1

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; Sequence 3, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match      81.6%; Score 161.5; DB 14; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 44

RESULT 3
US-10-855-068-3
; Sequence 3, Application US/10855068
; Publication No. US20040220106A1
; GENERAL INFORMATION:
; APPLICANT: Nelstuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/10/855,068
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US/09/302,239
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid
US-10-855-068-3

Query Match      81.6%; Score 161.5; DB 16; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 44

RESULT 4
US-09-782-587B-1
; Sequence 1, Application US/09782587B
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; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match      81.6%; Score 161.5; DB 10; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXQCQSFXXARXIFKDXARTKLFWISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
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; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa means 4-carboxylutamic acid (gamma-carboxylutamate)

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; TYPE: PRT
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 14
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication No. US20040143099A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jakob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

RESULT 15
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication No. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1

Query Match      81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXQCSPXXARXIFKDXARTKLFWISY 44

Search completed: August 22, 2005, 19:20:43
Job time : 662 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 92 Seconds
(without alignments)
189.176 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: 1 ANAYFLXLRPGSLRXCKX.....XXARXIFKDXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	84.9	408	7	ADf44980 Human Fac
2	161.5	81.2	44	2	AAY18305 Human fac
3	161.5	81.2	44	4	AAB36395 Human fac
4	161.5	81.2	44	7	ADD50096 Human vit
5	161.5	81.2	44	8	ADQ26902 Human fac
6	161.5	81.2	401	4	AAB84870 Mutant bl
7	161.5	81.2	401	4	AAB84871 Mutant bl
8	161.5	81.2	406	2	AAR35764 Factor VI
9	161.5	81.2	406	2	AAW14510 Modified
10	161.5	81.2	406	2	AAW14509
11	161.5	81.2	406	4	AAU77745 Human fac
12	161.5	81.2	406	4	AAB84867 Mutant bl
13	161.5	81.2	406	4	AAB84868 Mutant bl
14	161.5	81.2	406	4	AAB84869 Mutant bl
15	161.5	81.2	406	4	AAB84866 Wild-type
16	161.5	81.2	406	4	AAM52183 Human FVI
17	161.5	81.2	406	4	AAM52172 Mammalian
18	161.5	81.2	406	4	AAM52186 Human FVI
19	161.5	81.2	406	4	AAM52171 Human FVI
20	161.5	81.2	406	4	AAM52187 Human FVI
21	161.5	81.2	406	4	AAM52181 Human FVI
22	161.5	81.2	406	4	AAM52185 Human FVI
23	161.5	81.2	406	4	AAM52184 Human FVI
24	161.5	81.2	406	4	AAM52182 Human FVI
25	161.5	81.2	406	5	AAU77196 Human coa

26	161.5	81.2	406	5	AAU77191 Human coa
27	161.5	81.2	406	5	AAU77200 Human coa
28	161.5	81.2	406	5	AAU77192 Human coa
29	161.5	81.2	406	5	AAU77190 Human coa
30	161.5	81.2	406	5	AAU77198 Human coa
31	161.5	81.2	406	5	AAU77193 Human coa
32	161.5	81.2	406	5	AAU77199 Human coa
33	161.5	81.2	406	5	AAU79201 Human coa
34	161.5	81.2	406	5	AAU77188 Human coa
35	161.5	81.2	406	5	AAU77194 Human coa
36	161.5	81.2	406	5	AAU77195 Human coa
37	161.5	81.2	406	5	AAU77189 Human coa
38	161.5	81.2	406	5	AAU77197 Human coa
39	161.5	81.2	406	5	ABG31688 Human coa
40	161.5	81.2	406	5	ABB09178 Human fac
41	161.5	81.2	406	5	ABB80051 Human coa
42	161.5	81.2	406	5	ABB80069 Human coa
43	161.5	81.2	406	5	ABB80072 Human coa
44	161.5	81.2	406	5	ABB80071 Human coa
45	161.5	81.2	406	5	ABB80068 Human coa

ALIGNMENTS

RESULT 1
ADf44980
ID ADf44980 standard; protein; 408 AA.
XX
AC ADF44980;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human Factor VII variant, A3AY.
XX
KW Human; Factor VII; FVII; Factor VIIa; FVIIa; blood coagulation factor;
KW blood clotting disorder; brain haemorrhage; trauma; bleeding;
KW Haemostatic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4..5 /note= "Residues AY were inserted after position 3"
XX
PN WO2003093465-A1.
XX
PD 13-NOV-2003.
XX
PF 29-APR-2003; 2003WO-DK000276.
XX
PR 30-APR-2002; 2002US-0376679P.
XX
XX (MAXY-) MAXYGEN APS.
FA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Haaning JM, Andersen KV, Pedersen AH;
XX
DR WPI; 2003-903672/82.
XX
XX New Factor VII (FVII) or Factor VIIa (FVIIa) polypeptide variant, useful
PT in preparing a composition for treating a disorder where clot formation
PT is desirable, e.g., brain hemorrhages or blunt or penetrative trauma.
XX
PS Claim 13; Page; 78pp; English.
XX
CC The present invention relates to novel variants of Factor VII (FVII) or
CC Factor VIIa (FVIIa) protein. FVII is a blood coagulation factor. The
CC present sequence is a variant of the invention. The variants are useful
CC in preparing a composition for treating a disorder where clot formation
CC is desirable, e.g., brain haemorrhages, blunt or penetrative trauma, or
CC bleeding in patients undergoing living transplantations or resection or

CC variceal bleedings. Note: The present sequence is not shown in the
 CC specification, but was derived from information given in the wild-type
 CC human FVII sequence (ADP44971) and Claim 13.

XX
 SQ Sequence 408 AA;

Query Match 84.9%; Score 169; DB 7; Length 408;
 Best Local Similarity 76.7%; Pred. No. 3.6e-20;
 Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AYFLXLLRPGSLXRCXKXQCXFXARXIFKDXRTKLFWISY 45
 ||||| ||||| || ||||| ||||| ||||| ||||| |||||
 Db 4 AYFLEELRPGSLERECKEQCFEAREIFKDXRTKLFWISY 46

RESULT 2

AA18305
 ID AAY18305 standard; peptide; 44 AA.

XX
 AC AAY18305;

XX
 DT 17-AUG-1999 (first entry)

XX
 DE Human factor VII GLA domain.

XX
 KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Misc-difference 1. .44
 FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 acid"

XX
 PN WO9920767-A1.

XX
 PD 29-APR-1999.

XX
 PF 20-OCT-1998; 98WO-US022152.

XX
 PR 23-OCT-1997; 97US-00955636.

XX
 PA (MINU) UNIV MINNESOTA.

XX
 PI Nelsestuen GL;

XX
 DR WPI; 1999-288309/24.

XX
 PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 PT domain, useful for treating clotting disorders.

XX
 PS Disclosure; Page 15; 86pp; English.

XX
 CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain.
 CC The invention relates to a vitamin K-dependent polypeptide comprising a
 CC modified GLA domain containing an amino acid substitution which enhances
 CC membrane binding of the modified polypeptide as compared to the native
 CC polypeptide. The polypeptide is used to treat a clotting disorder by
 CC decreasing or increasing clot formation. Modification of the GLA domain
 CC results in a protein which has enhanced membrane binding affinity as
 CC compared to the native protein

XX
 SQ Sequence 44 AA;

Query Match 81.2%; Score 161.5; DB 2; Length 44;
 Best Local Similarity 97.8%; Pred. No. 7.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLLRPGSLXRCXKXQCXFXARXIFKDXRTKLFWISY 45
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 ANA-FLXLLRPGSLXRCXKXQCXFXARXIFKDXRTKLFWISY 44

RESULT 3

AA36395
 ID AAB36395 standard; peptide; 44 AA.

XX
 AC AAB36395;

XX
 DT 27-FEB-2001 (first entry)

XX
 DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.

XX
 KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
 KW clotting disorder; haemophilia A; haemophilia B; liver disease.

XX
 OS Homo sapiens.

XX
 PN WO20006753-A2.

XX
 PD 09-NOV-2000.

XX
 PF 28-APR-2000; 2000WO-US011416.

XX
 PR 29-APR-1999; 99US-00302239.

XX
 PA (MINU) UNIV MINNESOTA.

XX
 PI Nelsestuen GL;

XX
 DR WPI; 2001-007226/01.

XX
 PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and hemophilia, comprises modified gamma-
 PT carboxy glutamic acid domain that enhances membrane binding affinity.

XX
 PS Disclosure; Page 12; 81pp; English.

XX
 CC The present invention describes a vitamin K-dependent polypeptide (I)
 CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having at
 CC least one amino acid substitution, that enhances membrane binding
 CC affinity and the activity of the polypeptide relative to a corresponding
 CC native vitamin K-dependent polypeptide and inhibits clot formation. (I)
 CC can have thrombolytic and haemostatic activities, and can be used as an
 CC inhibitor of clot formation. (I) is useful for decreasing clot formation
 CC in a mammal, a factor VII or factor IX containing a modified GLA domain
 CC is useful for increasing clot formation and for treating a bleeding
 CC disorder, including thrombosis and clotting disorders such as haemophilia
 CC A, haemophilia B and liver disease. The present sequence represents a
 CC wild type human factor VII GLA domain sequence, given in the
 CC exemplification of the present invention

XX
 SQ Sequence 44 AA;

Query Match 81.2%; Score 161.5; DB 4; Length 44;
 Best Local Similarity 97.8%; Pred. No. 7.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLLRPGSLXRCXKXQCXFXARXIFKDXRTKLFWISY 45
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 ANA-FLXLLRPGSLXRCXKXQCXFXARXIFKDXRTKLFWISY 44

RESULT 4

ADD50096
 ID ADD50096 standard; protein; 44 AA.

XX
 AC ADD50096;

XX
 DT 15-JAN-2004 (first entry)

XX
 DE Human vitamin K-dependent protein #2.

XX

KW Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
KW GLA domain; membrane binding affinity; clot formation; haemophilia;
KW clotting disorder; site directed mutagenesis; haemostatic; anticoagulant;
KW thrombolytic.
XX
XX Homo sapiens.
XX
XX US2003100506-A1.
XX
XX 29-MAY-2003.
XX
XX 18-NOV-2002; 2002US-00298330.
XX
XX 23-OCT-1997; 97US-00955636.
XX 29-APR-1999; 99US-00302239.
XX 03-FEB-2000; 2000US-00497591.
XX
XX (NELS/) NELSESTUEN G L.
XX
XX Nelsestuen GL;
XX
XX WPI; 2003-606646/57.
XX
XX New vitamin K-dependent polypeptide for modulating clot formation in
XX mammals comprises a modified gamma-carboxyglutamic acid domain that
XX enhances membrane binding affinity and activity of the polypeptide.
XX
XX Example 5; SEQ ID NO 3; 51pp; English.
XX
XX The invention relates to a vitamin K-dependent polypeptide comprising a
XX modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane
XX binding affinity and activity of the polypeptide relative to a
XX corresponding native vitamin K-dependent polypeptide, where the modified
XX GLA domain comprises a glutamic acid residue at position 34. The
XX polypeptide is useful in modulating clot formation in mammals or in
XX treating certain types of haemophilia or clotting disorders. The membrane
XX binding affinity of polypeptides is increased by site directed
XX mutagenesis in the GLA domain. This sequence represents a vitamin K-
XX dependent protein of the invention.
XX
XX Sequence 44 AA;
Query Match 81.2%; Score 161.5; DB 7; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXRCXKXQCSPFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRCXKXQCSPFXXARXIFKDXRXTKLFWISY 44
RESULT 5
ADQ26902
ID ADQ26902 standard; protein; 44 AA.
XX
XX AC ADQ26902;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human factor VII gamma-carboxyglutamic acid (GLA) domain.
XX
XX Human; clot formation; protein C; activated protein C; APC;
KW gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;
KW aspirin; warfarin; heparin; haemophilic disorder; haemostatic;
KW anticoagulant; factor VII.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 1: 44
FT /label= OTHER
FT /note= "OTHER= All Xaa residues are glutamic acid or
FT gamma carboxyglutamic acid"

XX US6747003-B1.
XX 08-JUN-2004.
XX
XX 03-FEB-2000; 2000US-00497591.
XX
XX 23-OCT-1997; 97US-00955636.
XX 29-APR-1999; 99US-00302239.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 2004-429803/40.
XX
XX Decreasing clot formation by administering an anticoagulant agent, and a
XX protein C or activated protein C polypeptide having a modified GLA
XX domain, useful for treating hemophilic disorders in mammals.
XX
XX Example 5; SEQ ID NO 3; 41pp; English.
XX
XX The invention relates to a method of decreasing clot formation comprising
XX administering to a patient an anticoagulant agent and a protein C or
XX activated protein C (APC) polypeptide comprising a modified gamma-
XX carboxyglutamic acid (GLA) domain with two, three, four or five amino
XX acid substitutions. The invention also relates to vitamin K-dependent
XX nucleic acids, polypeptides, host cells, vectors and antibodies used in
XX the methods of the invention. The anticoagulant agent is aspirin,
XX warfarin or heparin, preferably aspirin. The methods and compositions of
XX the present invention are useful for modulating clot formation for
XX treating haemophilic disorders in mammals. This sequence represents the
XX human factor VII GLA domain, used in the method of the invention.
XX
XX Sequence 44 AA;
Query Match 81.2%; Score 161.5; DB 8; Length 44;
Best Local Similarity 97.8%; Pred. No. 7.2e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ANAYFLXXLRPGSLXRCXKXQCSPFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRCXKXQCSPFXXARXIFKDXRXTKLFWISY 44
RESULT 6
AAB84870
ID AAB84870 standard; protein; 401 AA.
XX
XX AC AAB84870;
XX
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-31).
XX
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
KW
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 311: 317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
XX
XX 13-MAR-2001.
XX
XX 24-AUG-1999; 99JP-00237610.
XX
XX 24-AUG-1999; 99JP-00237610.

XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX XX
 PS Claim 14; Page 20-21; 29pp; Japanese.
 XX XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX XX
 SQ Sequence 401 AA;
 Query Match 81.2%; Score 161.5; DB 4; Length 401;
 Best Local Similarity 75.6%; Pred. No. 6.9e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLXRXCKXQCQSFXXARXIFKDAERTKLFWISY 45
 Db 1 ANA-FLBELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 7
 AAB84871
 ID AAB84871 standard; protein; 401 AA.
 XX AC
 XX AAB84871;
 DT 31-JUL-2001 (first entry)
 XX XX
 DE Mutant blood coagulant factor VII (FVII-39).
 XX XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; muten.
 XX XX
 OS Homo sapiens.
 OS Synthetic.
 XX XX
 FH Key Location/Qualifiers
 FT Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 FT Misc-difference 311..317
 FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp -
 FT Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"
 XX XX
 PN JP2001061479-A.
 XX XX
 PD 13-MAR-2001.
 XX XX
 PF 24-AUG-1999; 99JP-00237610.
 XX XX
 PR 24-AUG-1999; 99JP-00237610.
 XX XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19464.
 XX XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX XX
 PS Claim 16; Page 23-24; 29pp; Japanese.
 XX XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients

XX SQ Sequence 401 AA;
 Query Match 81.2%; Score 161.5; DB 4; Length 401;
 Best Local Similarity 75.6%; Pred. No. 6.9e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLXRXCKXQCQSFXXARXIFKDAERTKLFWISY 45
 Db 1 ANA-FLBELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 8
 AAR35764
 ID AAR35764 standard; protein; 406 AA.
 XX AC
 XX AAR35764;
 DT 25-MAR-2003 (revised)
 DT 24-SEP-1993 (first entry)
 XX XX
 DE Factor VII (VII).
 XX XX
 KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
 KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite;
 KW catalytic activity.
 XX XX
 OS Homo sapiens.
 XX XX
 FH Key Location/Qualifiers
 FT Region 1..152
 FT /note= "Factor VII light chain"
 FT Region 153..406
 FT /note= "Factor VII heavy chain"
 FT Peptide 245..266
 FT /note= "Claim 9, page 138-139 describes an antibody that
 FT reacts with Factor VII; fragments 289-304, 290-304, 290-
 FT 310, 374-388 and 400-414 but not with fragment 245-266"
 FT Peptide 289..304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 290..310
 FT /note= "exosite 2"
 FT Peptide 290..310
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 FT Peptide 290..304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 374..388
 FT /note= "exosite 1"
 FT Peptide 374..388
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 XX XX
 PN WO9309804-A1.
 XX XX
 PD 27-MAY-1993.
 XX XX
 PF 18-NOV-1992; 92WO-US010242.
 XX XX
 PR 18-NOV-1991; 91US-00793989.
 XX XX
 PA (SCRI) SCRIPPS RES INST.
 XX XX
 PI Griffin JH, Meesters RM;
 XX XX
 DR WPI; 1993-182244/22.
 XX XX
 PT Serine protease derived-polypeptide(s) and anti-peptide antibodies - for
 PT inhibiting coagulation and assaying for the presence of serine protease
 PT in fluid samples.
 XX XX
 PS Disclosure; Page 133-135; 149pp; English.
 XX XX
 CC The PC polypeptides indicated in the Features Table inhibit coagulation
 CC (they prevent binding of serine protease to natural substrates), esp.

CC when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-
CC 10) microm. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are
CC described in the specification but have not yet been added to the
CC SEQUENCE LISTING. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 406 AA;

Query Match 81.2%; Score 161.5; DB 2; Length 406;
Best Local Similarity 75.6%; Pred. NO. 7e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRCSLXXCKXQCSFXXARXIFKDAKTKLFWISY 45
Db 1 ANA-FLESLRPGSLRECKEQCSPEAREIFKDAERTKLFWISY 44

RESULT 9
AAW14510
ID AAW14510 standard; protein; 406 AA.
XX
AC AAW14510;
XX
XX 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
DE Modified blood coagulation Factor VII (R315S).
XX
XX Blood coagulation; factor 7; mutein; mutation; modification;
KW thrombocytopenia; von Willebrand's disease; plasma substitute.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 6
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 14
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 16
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 17. .22
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 19
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 25
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32. .33
FT /note= "proteolytic site"
FT Modified-site 35
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 38. .39
FT /note= "proteolytic site"
FT Cleavage-site 42. .43
FT /note= "proteolytic site"
FT Cleavage-site 44. .45
FT /note= "proteolytic site"

FT Disulfide-bond 50. .61
FT Disulfide-bond 55. .70
FT Modified-site 63
FT /label= OTHER
FT /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72. .81
FT Disulfide-bond 91. .102
FT Disulfide-bond 98. .112
FT Disulfide-bond 114. .127
FT Disulfide-bond 135. .162
FT Cleavage-site 143. .144
FT /note= "proteolytic site"
FT Modified-site 145
FT /note= "glycosylation site"
FT Disulfide-bond 159. .164
FT Disulfide-bond 178. .194
FT Active-site 193
FT Active-site 242
FT Cleavage-site 290. .291
FT /note= "proteolytic site"
FT Disulfide-bond 310. .329
FT Cleavage-site 315. .316
FT /note= "proteolytic site in unmodified factor VII"
FT Misc-difference 315
FT /note= "native Arg315 has been substituted by Ser to
FT provide a proteolytically more stable peptide bond"
FT Modified-site 322
FT /note= "glycosylation site"
FT Disulfide-bond 340. .368
FT Cleavage-site 341. .342
FT /note= "proteolytic site"
FT Active-site 344
FT Cleavage-site 392. .393
FT /note= "proteolytic site"
FT Cleavage-site 396. .397
FT /note= "proteolytic site"
FT Cleavage-site 402. .403
FT /note= "proteolytic site"
XX US5580560-A.
XX
XX 03-DEC-1996.
XX
XX 22-AUG-1994; 94US-00293778.
XX
XX 13-NOV-1989; 89US-00434149.
XX 12-JUN-1992; 92US-00898248.
XX 09-AUG-1993; 93US-00104509.
XX (NOVO) NOVO-NORDISK AS.
XX
XX Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
XX WPI; 1997-033523/03.
XX
XX Mutated human factor VII or VIIa proteins - with amino acid substitutions
XX to improve proteolytic stability.
XX
XX Example 4; Page; 28pp; English.
XX
XX Modified human factor VII or VIIa proteins are stabilised against
XX proteolytic cleavage by substitution of one of the residues Lys32, Lys38,
XX Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an
XX amino acid that provides a proteolytically more stable peptide bond,
XX provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
XX The modified proteins are useful for treating bleeding disorders such as
XX thrombocytopenia and von Willebrand's disease. They are also suitable for
XX addition to plasma substitutes. The present sequence is a specific
XX example of a modified factor VII protein. (Updated on 25-MAR-2003 to
XX correct PP field.)
SQ Sequence 406 AA;


```

RESULT 12
AAB84867
ID AAB84867 standard; protein; 406 AA.
XX AC
XX AAB84867;
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-5).
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 159 /note= "Wild-type Cys substituted by Ala"
XX FT
XX Misc-difference 164 /note= "Wild-type Cys substituted by Ala"
XX FT
XX
XX JP2001061479-A.
XX PN
XX 13-MAR-2001.
XX PD
XX PF 24-AUG-1999; 99JP-00237610.
XX PR 24-AUG-1999; 99JP-00237610.
XX PS
XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX PA
XX WPI; 2001-310677/33.
XX DR N-PSDB; AAH19460.
XX DT
XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
XX the treatment of hemophilia.
XX PS Claim 3; Page 11-12; 29pp; Japanese.
XX CC The present invention relates to mutants of blood coagulant factor VII
XX (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX sequence is one such mutant FVII: VII-5. In the wild-type protein
XX (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
XX protein, the disulphide bond is disrupted. The mutance can be used as an
XX agent for the substitution therapy of haemophilia inhibitor patients
XX
XX Sequence 406 AA;
XX Query Match 81.2%; Score 161.5; DB 4; Length 406;
XX Best Local Similarity 75.6%; Pred. NO. 7e-19;
XX Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1
XX
XX Qy 1 ANAYFLXLRPGSLRXKXXQCSFXRXRXIFKDXRTKLFWSY 45
XX ||| || ||||| || ||||| ||||| ||||| ||||| |||||
XX Db 1 ANA-FLELRPGSLRECKEQCSFEAREIFKDAERTKLFWSY 44
XX ||| || ||||| || ||||| ||||| ||||| ||||| |||||
XX
XX RESULT 13
XX AAB84868
XX ID AAB84868 standard; protein; 406 AA.
XX AC
XX AAB84868;
XX 31-JUL-2001 (first entry)
XX
XX Mutant blood coagulant factor VII (FVII-6).
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX mutant; mutein.
XX Homo sapiens.

```

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 164
 FT /note= "Wild-type Cys substituted by Ala"
 FT Misc-difference 299
 FT /note= "Wild-type Val substituted by Cys"
 XX
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19461.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Claim 5; Page 14-15; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-6. In the wild-type protein
 CC (AAB84866), there is a disulphide bond (159Cys-164Cys). In the present
 CC protein, the disulphide bond is disrupted. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXKCKXXQCSCFXRXKXIFKDAKRTKLFWISY 45
 Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 14
 AAB84869
 ID AAB84869 standard; protein; 406 AA.
 AC AAB84869;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Mutant blood coagulant factor VII (FVII-30).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 XX mutant; mutein.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 235..239
 FT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
 FT Arg-Lys-Thr-Leu"
 FT
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Claim 9; Page 17-18; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-30. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXKCKXXQCSCFXRXKXIFKDAKRTKLFWISY 45
 Db 1 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 44
 RESULT 15
 AAB84866
 ID AAB84866 standard; protein; 406 AA.
 XX
 XX AAB84866;
 XX
 XX 31-JUL-2001 (first entry)
 XX
 XX Wild-type human blood coagulant factor VII (FVII).
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 159..164
 FT
 XX JP2001061479-A.
 XX
 XX 13-MAR-2001.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX 24-AUG-1999; 99JP-00237610.
 XX
 XX (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX WPI; 2001-310677/33.
 DR N-PSDB; AAH19459.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 XX Disclosure; Page 8-9; 29pp; Japanese.
 XX
 XX The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence represents the protein sequence for wild-type human FVII. The
 CC mutants can be used as an agent for the substitution therapy of
 CC haemophilia inhibitor patients
 XX
 XX Sequence 406 AA;
 SQ
 Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy	1	ANAYFLXXLRPGSLRXCKXCXOCSEXXARXIFKDAERTKLFWISY	45
Db	1	ANA-FLEELRPGSLERECKEEOCSFEAREIFKDAERTKLFWISY	44

Search completed: August 22, 2005, 18:45:41
Job time : 93 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 25 Seconds
(without alignments)
173.190 Million cell updates/sec

Title: US10031005-3Y4
Perfect score: 199
Sequence: 1 ANAYFLXXLRPGSLRXCKX.....XXARXIFDXARTKLFWISY 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	466	1 KFHU7	coagulation factor
2	127.5	64.1	443	2 I46932	coagulation factor
3	113	56.8	407	1 KPB07	coagulation factor
4	98.5	49.5	461	1 JX0210	protein C (activat
5	93.5	47.0	456	1 KXBO	protein C (activat
6	91.5	46.0	488	1 EXHU	coagulation factor
7	90.5	45.5	492	1 EXBO	coagulation factor
8	89.5	45.0	461	1 S18994	protein C (activat
9	88.5	44.5	482	1 EXRT	coagulation factor
10	86	43.2	416	1 KPE0	coagulation factor
11	86	43.2	617	2 S10511	thrombin (EC 3.4.2
12	86	43.2	618	2 A35827	thrombin (EC 3.4.2
13	83	41.7	461	1 KFHU	coagulation factor
14	80.5	40.5	475	1 EXCH	coagulation factor
15	78	39.2	452	1 A30351	coagulation factor
16	78	39.2	459	2 JQ0419	coagulation factor
17	75	37.7	396	1 KXBOZ	plasma protein 2 -
18	73.5	36.9	461	1 KKHU	protein C (activat
19	73	36.7	622	1 TBHU	thrombin (EC 3.4.2
20	70	35.2	422	1 KKHUZ	plasma protein 2 p
21	69	34.7	625	1 TBBO	thrombin (EC 3.4.2
22	61.5	30.9	576	2 G56763	probable MAP kinas
23	61	30.7	594	2 D84859	probable MAP kinas
24	61	30.7	603	2 C96575	probable MAP kinas
25	58.5	29.4	642	2 S53433	plasma protein S p
26	56	28.1	675	1 KXBOS	plasma protein S p
27	55.5	27.9	675	1 KXMS	plasma protein S p
28	55	27.6	673	2 A48089	growth arrest-spec
29	53.5	26.9	642	2 S53434	plasma protein S p

30 53.5 26.9 646 2 S38819 plasma protein S -
31 53.5 26.9 676 1 KXHUS plasma protein S p
32 53 26.6 674 2 I55476 growth potentiatin
33 53 26.6 675 1 KXRTS plasma protein S p
34 53 26.6 678 2 B48089 growth arrest-spec
35 47.5 23.9 319 2 T15137 hypothetical prote
36 46.5 23.4 516 2 H84424 probable MAP kinas
37 46 23.1 514 2 C64154 hypothetical prote
38 46 23.1 543 2 H84724 probable ARI-like
39 45 22.6 879 2 S55864 hypothetical prote
40 44 22.1 226 2 E96531 hypothetical prote
41 43.5 21.9 367 2 B56598 hypothetical kinase
42 43.5 21.9 385 2 T15221 hypothetical prote
43 43.5 21.9 1298 2 A48999 protein-tyrosine k
44 43.5 21.9 1363 2 I58375 protein-tyrosine k
45 43.5 21.9 1379 2 JC4954 vascular endotheli

RESULT 1
KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: A28322; A23819; A31186; B31186; S63524
R:O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, F.S.; Murze
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende
A:Reference number: A28322; MUID:87260948; PMID:3037537
A:Accession: A28322
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: UNIPROT:P08709; GB:J02933; NID:gl80333; PIDN:AAA51983.1; PID:gl80334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:W13232; NID:gl82799; PIDN:AAA88040.1; PID:gl82801
R:Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
A:Residues: 213-466 <TH2>
R:Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peders
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at
A:Reference number: A40529; MUID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
R:Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A:Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy
A:Reference number: S63524; MUID:96096752; PMID:8529655
A:Accession: S63524
A:Molecule type: protein
A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C:Genetics:
A:Gene: GDB:F7
A:Cross-references: GDB:119897; OMIM:227500
A:Map position: 13q34-13q34
A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser
coagulation factor IX in the presence of calcium and tissue factor

ALIGNMENTS

A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-60/Domain: propeptide #status predicted <PRO>
F;45-104/Domain: Gla domain homology <GLA>
F;61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;110-141/Domain: EGF homology <EG1>
F;151-187/Domain: EGF homology <EG2>
F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;213-447/Domain: trypsin homology <TRY>
F;66,67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;77-82,110-121,115-130,132-141,152-162,158-172,174-187,195-322,219-224,238-254,370-389,
F;112,120/Binding site: carboxylate (Ser) (covalent) #status experimental
F;123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F;205,382/Binding site: carboxylate (Asn) (covalent) #status experimental
F;212-213/Cleavage site: carboxylate (Asp) (covalent) #status experimental
F;212-213/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;253,302,404/Active site: His, Asp, Ser #status predicted
F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 81.2%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 2.5e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWSY 45
Db 61 ANA-FLBRLPGSLERECKEQCSFEAREIFKDAERTKLFWSY 104

RESULT 2
146932
coagulation factor VII - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C;Accession: I46932
R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A;Reference number: I46932; MUID:93190306; PMID:838365
A;Accession: I46932
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-443 <BRO>
A;Cross-references: GB:S56300; NID:g266294; PID:g266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F;89-120/Domain: Gla domain homology <GLA>
F;89-120/Domain: EGF homology <EG1>
F;130-166/Domain: EGF homology <EG2>
F;192-425/Domain: trypsin homology <TRY>

Query Match 64.1%; Score 127.5; DB 2; Length 443;
Best Local Similarity 57.8%; Pred. No. 1.4e-13;
Matches 26; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWSY 45
Db 40 ANS-FLBRLPGSLERECKEQCSFEAREVFQSTERTKQFWY 83

RESULT 3
KFB07
coagulation factor VIIa (EC 3.4.21.21) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A31979; C20274
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Reference number: A31979; MUID:89008362; PMID:3049594
A;Accession: A31979
A;Molecule type: protein
A;Residues: 1-407 <TAK>
A;Cross-references: UNIPROT:P22457

R;McMullen, B.A.; Fujikawa, K.; Kiesel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VII.
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Accession: C20274
A;Molecule type: protein
A;Residues: 58-62, 'X', 64-68 <MCM>
A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
J. Biochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VII.
A;Reference number: A45556; MUID:89213999; PMID:3149637
A;Contents: annotation
A;Note: structure and location of covalently bound carbohydrate
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
A;Pathway: blood coagulation extrinsic pathway
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F;1-44/Domain: Gla domain homology (fragment) <GLA>
F;50-81/Domain: EGF homology <EG1>
F;91-127/Domain: EGF homology <EG2>
F;153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;153-387/Domain: trypsin homology <TRY>
F;6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;17-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/I
F;52/Binding site: carboxylate (Ser) (covalent) #status experimental
F;63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
F;145,203/Binding site: carboxylate (Asn) (covalent) #status experimental
F;152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental
F;193,242,344/Active site: His, Asp, Ser #status predicted
F;290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 56.8%; Score 113; DB 1; Length 407;
Best Local Similarity 51.2%; Pred. No. 3.6e-11;
Matches 21; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 5 FLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWSY 45
Db 4 FLBRLPGSLERECKEQCSFEAREVFQSTERTKQFWY 44

RESULT 4
JX0210
protein C (activated) (EC 3.4.21.69) precursor - mouse
N;Alternate names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JX0210
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
J. Biochem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
A;Accession: JX0210
A;Molecule type: mRNA
A;Residues: 1-461 <TAD>
A;Cross-references: UNIPROT:P33587; GB:D10445; NID:g220385; PID:BAA01235.1; PID:g220386
A;Experimental source: liver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that regulates blood coagulation
S.
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-33/Domain: signal sequence #status predicted <SIG>
F;27-85/Domain: Gla domain homology <GLA>
F;34-41/Domain: propeptide #status predicted <PRO>
F;42-196,199-461/Product: protein C #status predicted <PCR>
F;42-196/Domain: light chain #status predicted <PCL>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;199-461/Domain: heavy chain #status predicted <PCH>
F;199-211/Domain: activation peptide #status predicted <ACT>

F;30-39/Domain: propeptide #status predicted <PRO>
F;40-194/Product: protein c light chain #status experimental <LCH>
F;98-128/Domain: EGF homology <EG1>
F;137-172/Domain: EGF homology <EG2>
F;197-456/Product: protein C heavy chain #status experimental <HCH>
F;197-210/Domain: activation peptide #status experimental <APT>
F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Diulfide bonds: #stat
F;136,289,350/Binding site: carbohydrate (Aasn) (covalent) #status predicted
F;252,298,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carbohydrate (Aasn) (covalent) #status predicted

Query Match 47.0%; Score 93.5; DB 1; Length 456;
Best Local Similarity 44.4%; Pred. No. 8.1e-08;
Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRPGSLXRXCKXCQCSPFXKARXIPKDAXRTKLFWISY 45
||| ||||||| : | | | | | | | | | | | |
Db 40 ANS-FLBELRPGNVERECSEBVCPEAREIFQNTEDTMAFWFSY 83

RESULT 6

EXHU
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
N;Alternate names: Stuart factor
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text change 09-Jul-2004
C;Accession: A24478; JQ0917; A2485; A25853; A22208; A21284; A20362; S39415; I54051; A00
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is
A;Reference number: A24478; MUID:87026600; PMID:3768336
A;Accession: A24478
A;Molecule type: DNA
A;Residues: 1-488 <LEY>
A;Cross-references: UNIPROT:P00742; GB:L29433; GB:M14327; NID:G459809; PIDN:AAAS2764.1; I
R;Wessler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagu
A;Reference number: JQ0917; MUID:91216473; PMID:1902434
A;Accession: JQ0917
A;Molecule type: mRNA
A;Residues: 1-488 <MES>
A;Cross-references: GB:M57285; NID:G182389; PIDN:AAAS2421.1; PID:G182390
R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagulati
A;Reference number: A42485; MUID:92218390; PMID:1313796
A;Accession: A42485
A;Molecule type: DNA
A;Residues: 1-15 <MTA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X CDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
A;Accession: A25853
A;Molecule type: mRNA
A;Residues: 19-284, 'E' 289-488 <KAU>
A;Cross-references: GB:M22613; NID:G180335; PIDN:AAA51984.1; PID:G180336
R;Fung, M.R.; Hay, C.W.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of an almost full-length cDNA coding for human blood coagulat
A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Accession: A22208
A;Molecule type: mRNA
A;Residues: 13-441, 'S' 443-488 <FUN>
A;Cross-references: GB:X03194; NID:G182840; PIDN:AAA52490.1; PID:G182841
R;Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:84222026; PMID:6587384
A;Accession: A21284
A;Molecule type: mRNA
A;Residues: 13-284, 'E', 289-488 <LE2>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weine Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A;Reference number: A20362; MUID:8325207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
A;Residues: 41-179 <MCM>
R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X.
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39415
A;Molecule type: protein
A;Residues: 183-234 <INO>
A;Note: Glycosylation sites
A;Note: Identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G. Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.
A;Reference number: 154051; MUID:90128299; PMID:2612918
A;Accession: 154051
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:W33287; NID:G183860; PIDN:AAA52636.1; PID:G553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blass J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
A;Reference number: A49458; MUID:93360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-chain polypeptide.
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or factor XIa.
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: GDB:119890; OMIM:227600
A;Map position: 13q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of factor V.
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;41-179/Product: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;235-488/Product: coagulation factor X heavy chain #status experimental <ACT>
F;235-462/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F;57-62/Disulfide bonds: #status predicted
F;90-101,95-101,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;199,211/Binding site: carboxyglutamate (Thr) (covalent) #status experimental
F;221,231/Binding site: carboxyglutamate (Asn) (covalent) #status experimental
F;224-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status experimental
F;276,322,419/Active site: His, Asp, Ser #status experimental

Query Match 46.0%; Score 91.5; DB 1; Length 488;
Best Local Similarity 40.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
Qy 1 ANAYFLXLRGSLXRCXKXQCFFXXARXIFDKAXTKLFWISY 45

Db 41 ANS-FLEEMKKGHLERCMBETCSYBEAREVFDSDKNTNEFWNKY 84
RESULT 7
EXBO
coagulation factor Xa (BC 3.4.21.6) precursor - bovine
N;Alternate names: Stuart factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A. Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a signal peptide.
A;Reference number: A22867; MUID:84247315; PMID:6330671
A;Accession: A22867
A;Molecule type: mRNA
A;Residues: 1-487 <FUN>
A;Cross-references: UNIPROT:P00743; GB:X00673; NID:G192; PIDN:CAA25286.1; PID:G193
R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K. Biochemistry 19, 659-667, 1980
A;Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A;Reference number: A14997; MUID:80130563; PMID:6766735
A;Accession: A14997
A;Molecule type: protein
A;Residues: 41-102, 'N', 104-180 <ENF>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.
A;Reference number: A20274; MUID:83308813; PMID:6688526
A;Contents: annotation; revision to residue 103
R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H. Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A;Reference number: A12030; MUID:76053089; PMID:1059093
A;Accession: A12030
A;Molecule type: protein
A;Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GRKG',446-492 <TJ>
A;Note: carboxydrate binding sites and disulfide bonds were determined
R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J. J. Biol. Chem. 264, 16897-16904, 1989
A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal factor X.
A;Reference number: A34412; MUID:89380326; PMID:2789221
A;Accession: A34412
A;Molecule type: protein
A;Residues: 85-126 <PER>
A;Note: beta-hydroxyaspartic acid site
R;Inoue, K.; Morita, T. Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of factor X.
A;Reference number: S39414; MUID:94062825; PMID:8243461
A;Accession: S39414
A;Molecule type: protein
A;Residues: 183-196;199-209;216-233 <INO>
A;Note: carboxydrate binding sites
R;Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; DeWitt, D.L. Biochemistry 11, 4899-4903, 1972
A;Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian factor X.
A;Reference number: A12453; MUID:73053314; PMID:4264286
A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davies, E.W. Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to factor Xb.
A;Reference number: A13504; MUID:76053121; PMID:1059122
A;Contents: annotation; activation
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J. J. Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid residue.
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.W. J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800

F;43-461/Product: protein C #status predicted <PRC>
F;91-130/Domain: EGF homology <EG1>
F;139-174/Domain: EGF homology <EG2>
F;213-445/Domain: trypsin homology <TRY>
F;47, 48, 55, 57, 60, 61, 66, 67, 70, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status I
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #stat
F;215,291,355/Binding site: carboxylate (Asn) [covalent] #status predicted
F;254,300,402/Active site: His, Asp, Ser #status predicted

Query Match 45.0%; Score 89.5; DB 1; Length 461;
Best Local Similarity 44.4%; Pred. No. 3.9e-07;
Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRPGSLRXRCXQCXQCSFXRXARXIFKDXRTKLFWISY 45
||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 42 ANS-FLEEVAGSLERECMEIEICDFEBAQEIQFNVEDTLAFWKY 85

RESULT 9
EXRT
coagulation factor Xa (BC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: S49075; Jc4670; PS0191; PS0190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intrac
A:Reference number: A58498; MUID:96093366; PMID:8578539
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STA2>
A:Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g50660
A>Note: submitted to the EMBL Data Library, June 1994
A>Note: neither the complete nucleic acid sequence nor the complete translation are show
R:Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: JC4670; MUID:96194815; PMID:8647460
A:Accession: JC4670
A:Molecule type: mRNA
A:Residues: 1-482 <STA2>
A:Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
A:Experimental source: Cos-1 cell
R:Enjoji, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plas
A:Reference number: PS0190; MUID:92041742; PMID:1718949
A:Accession: PS0191
A:Molecule type: protein
A:Residues: 41-58,'X',60-65 <ENJ1>
A:Accession: PS0190
A:Molecule type: protein
A:Residues: 183-186,'X',188-207 <ENJ2>
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of t
A:Reference number: I46196; MUID:94222160; PMID:8168596
A:Accession: I62745
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 295-383,'G',385-455 <MUR>
A:Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;25-84/Domain: Gla domain homology <GLA>
F;1-179/Product: coagulation factor X light chain #status predicted <LCH>
F;90-121/Domain: EGF homology <EGI>

A:Accession: A30511
A:Molecule type: DNA
A:Residues: 8-24 <REI>
A:Cross-references: EMBL:X55008; NID:G311288; PIDN:CAB38245.2; PID:G4469253
R:Koerber, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
Am J Hum. Genet. 45, 448-457, 1989
A:Title: Functionally important regions of the factor IX gene have a low rate of polymorphism
A:Reference number: A32989; MUID:89371752; PMID:2773937
A:Accession: A32989
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 30-92 <ROE>
R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
A:Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulation
A:Reference number: A22673; MUID:85190593; PMID:3857619
A:Accession: A22673
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <MCG>
A:Cross-references: GB:M11309; NID:g180552; PIDN:AAA52023.1; PID:g180553
A:Note: the authors translated the codon ACA for residue 29 as Tyr
R:Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstoshe
Nucleic Acids Res. 11, 2325-2335, 1983
A:Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
A:Reference number: A21337; MUID:83220788; PMID:6687940
A:Accession: A21337
A:Molecule type: mRNA
A:Residues: 1-193, 'T', 195-461 <JAY>
A:Cross-references: GB:J00137; NID:g182610; PIDN:AAA52763.1; PID:g182611
R:Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
Somat. Cell Mol. Genet. 10, 465-473, 1984
A:Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
A:Reference number: A37546; MUID:84300526; PMID:6089357
A:Accession: A37546
A:Molecule type: mRNA
A:Residues: 38-193, 'T', 195-326 <JAG>
A:Cross-references: GB:M135672
R:Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A:Title: Isolation and characterization of a cDNA coding for human factor IX.
A:Reference number: A30623; MUID:83065193; PMID:6959130
A:Accession: A30623
A:Molecule type: mRNA
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A', i
A:Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609
A:Experimental source: liver
R:Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
Vox Sang. 58, 21-29, 1990
A:Title: Development of an immunoaffinity process for factor IX purification.
A:Reference number: A60486; MUID:90194857; PMID:2316207
A:Accession: A60486
A:Molecule type: protein
A:Residues: 47-52, 'X', 55-60, 'X', 62, 'X', 65 <THA>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: A20274
A:Molecule type: protein
A:Residues: 105-109, 'X', 111-115 <MCM>
R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle
Eur. J. Biochem. 172, 565-572, 1988
A:Title: Characterization of two differently processed forms of human recombinant factor
A:Reference number: S02527; MUID:88166735; PMID:3280312
A:Accession: S02527
A:Molecule type: protein
A:Residues: 29-63 <BAL>
A:Note: processed forms expressed in recombinant system
R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien, I
EMBO J. 9, 3295-3303, 1990
A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and
A:Reference number: S12058; MUID:91006024; PMID:2209546
A:Accession: S12058

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 83 Seconds
(without alignments)
277.633 Million cell updates/sec

Title: US10031005-3y4

Perfect score: 199

Sequence: 1 ANAYFLXLRPGSLRXCKX.....XXARXIFDAXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	161.5	81.2	466 1 FA7_HUMAN	P08709 homo sapien
2	161.5	81.2	679 2 Q96P08	Q96P08 homo sapien
3	127.5	64.1	444 1 FA7_RABIT	P98139 oryctolagus
4	116.5	58.5	446 1 FA7_MOUSE	P70375 mus musculus
5	113	56.8	407 1 FA7_BOVIN	P22457 bos taurus
6	109	54.8	443 2 Q80HC9	Q80HC9 brachydanio
7	103.5	52.0	459 1 PRTC_FIG	Q96IP2 sus scrofa
8	98.5	49.5	460 1 PRTC_MOUSE	P33587 mus musculus
9	96	48.2	179 2 Q8TAS3	Q8TAS3 homo sapien
10	96	48.2	198 1 TMG2_MOUSE	Q8T182 mus musculus
11	96	48.2	202 1 TMG2_HUMAN	O14669 homo sapien
12	95	47.7	216 2 Q6DIH4	Q6DIH4 xenopus tro
13	94	47.2	442 2 Q804X1	Q804X1 figu rubrip
14	93.5	47.0	425 2 Q804X7	Q804X7 gallus gall
15	93.5	47.0	446 1 FA7_RAT	Q8K3U6 rattus norv
16	93.5	47.0	456 1 PRTC_BOVIN	P00745 bos taurus
17	92	46.2	208 2 Q6GPL7	Q6GPL7 xenopus lae
18	92	46.2	537 2 Q804W8	Q804W8 figu rubrip
19	91.5	46.0	218 1 TMG1_HUMAN	O14668 homo sapien
20	91.5	46.0	266 2 Q8NEK6	Q8NEK6 homo sapien
21	91.5	46.0	488 1 FA10_HUMAN	P00742 homo sapien
22	90.5	45.5	492 1 FA10_BOVIN	P00743 bos taurus
23	89.5	45.0	461 1 PRTC_RAT	P31394 rattus norv
24	88.5	45.0	461 2 Q68FY8	Q68FY8 rattus norv
25	88.5	44.5	433 2 Q804X5	Q804X5 gallus gall
26	88.5	44.5	469 2 Q9GMD9	Q9GMD9 ornithorhyn
27	88.5	44.5	482 1 FA10_RAT	Q63207 rattus norv
28	88	44.2	471 2 Q804X6	Q804X6 gallus gall
29	87.5	44.0	490 1 FA10_RABIT	O15045 oryctolagus
30	87	43.7	226 1 TMG4_HUMAN	Q9BZD6 homo sapien
31	86.5	43.5	340 2 Q80Y26	Q80Y26 mus musculus

32	86.5	43.5	376 1 FA10_TROCA	P81428 tropidechia
33	86.5	43.5	432 2 Q6GNA2	Q6GNA2 xenopus lae
34	86.5	43.5	481 1 FA10_MOUSE	Q88947 mus musculus
35	86	43.2	49 2 Q95ME8	Q95ME8 bos taurus
36	86	43.2	416 1 FA9_BOVIN	P00741 bos taurus
37	86	43.2	617 1 THR8_RAT	P18292 rattus norv
38	86	43.2	618 1 THR8_MOUSE	P19221 mus musculus
39	85.5	43.0	524 2 Q7SXH8	Q7SXH8 brachydanio
40	85	42.7	434 2 Q7T3B6	Q7C3B6 brachydanio
41	84.5	42.5	376 1 FA10_HOPST	P83370 hoplocephal
42	83.5	42.0	458 1 PRTC_RABIT	Q28661 oryctolagus
43	83.5	42.0	462 2 Q6PAG2	Q6PAG2 xenopus lae
44	83	41.7	455 2 Q7SY86	Q7SY86 xenopus lae
45	83	41.7	461 1 FA9_HUMAN	P00740 homo sapien

ALIGNMENTS

RESULT 1
FA7_HUMAN
ID FA7_HUMAN STANDARD; PRT; 466 AA.
AC P08709; Q14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (SPCA) (Proconvertin) (Eptacog alfa).
GN Name=F7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.B., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K., Davie E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;
RT "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
[3]
RN SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RA MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";
RL Biochemistry 27:7785-7793(1988).
[5]
RN CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RA MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kisiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine.";

RL J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimomura Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";
RT J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/380041a0;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
RN [10]
RP STRUCTURE BY NMR OF 105-145.
RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
RA Drakenberg T.;
RT "Solution structure of the N-terminal EGF-like domain from human factor VII.";
RL Biochemistry 37:10605-10615(1998).
RN [11]
RP VARIANT GLN-364.
RX MEDLINE=91300046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RT "Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected male.";
RL Blood 78:132-140(1991).
RN [12]
RP VARIANTS GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patraccini P., Gemmati D., Derosa V., Pinotti M.,
RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
RT "Detection of two missense mutations and characterization of a repeat polymorphism in the factor VII gene (F7)." ;
RL Hum. Genet. 89:497-502(1992).
RN [13]
RP VARIANT TYR-238.
RX MEDLINE=93372811; PubMed=8364544;
RA Marchetti G., Ferrati M., Patraccini P., Redaelli R., Bernardi F.;
RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms (115His and 333Ser) in the human coagulation factor VII gene.";
RL Hum. Mol. Genet. 2:1055-1056(1993).
RN [14]
RP VARIANTS.
RX MEDLINE=94061028; PubMed=8242057;
RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,
RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
RA Tuddenham E.G.D., McVey J.H.;
RT "Detection of missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of

RT coagulation factor VII.";
RL Hum. Mol. Genet. 2:1355-1359(1993).
RN [15]
RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
RX MEDLINE=94284305; PubMed=8204879;
RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
RT "Severe factor VII deficiency caused by mutations abolishing the cleavage site for activation and altering binding to tissue factor.";
RL Blood 83:3524-3535(1994).
RN [16]
RP VARIANT SER-367.
RX PubMed=7860081;
RA Dewald G., Noehle M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of human complement component C7.";
RL Hum. Hered. 44:301-304(1994).
RN [17]
RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7981691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RT "Topologically equivalent mutations causing dysfunctional coagulation factors VII (294Ala-->SVal) and X (334Ser-->Pro)." ;
RL Hum. Mol. Genet. 3:1175-1177(1994).
RN [18]
RP VARIANT MIE HIS-307.
RX MEDLINE=95064662; PubMed=7974346;
RA Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RT "Factor VII M1e: homozygous asymptomatic type I deficiency caused by an amino acid substitution of His (CAC) for Arg(247) (CGC) in the catalytic domain.";
RL Thromb. Haemost. 71:773-777(1994).
RN [19]
RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbini A.A., Mannucci P.M., Bauer K.A.;
RT "A Thr359Met mutation in factor VII of a patient with a hereditary deficiency causes defective secretion of the molecule.";
RL Blood 87:5085-5094(1996).
RN [20]
RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RX DOI=10.1002/(SICI)1098-1004(1996)8:2<108::AID-HUMU2>3.3.CO;2-6;
RA Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RT "Mutation pattern in clinically asymptomatic coagulation factor VII deficiency.";
RL Hum. Mutat. 8:108-115(1996).
RN [21]
RP VARIANT VAL-304.
RX MEDLINE=97037613; PubMed=8883260;
RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zaizov R.,
RA Seligsohn U.;
RT "Ala244Val is a common, probably ancient mutation causing factor VII deficiency in Moroccan and Iranian Jews.";
RL Thromb. Haemost. 76:283-291(1996).
RN [22]
RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with factor VII deficiency.";
RL Br. J. Haematol. 101:47-49(1998).
RN [23]
RP VARIANTS MALTA THR-194 AND VAL-304.
RX MEDLINE=98112461; PubMed=9452082;
RA Alshinawi C., Scerri C., Gaidies R., Aquilina A., Felice A.E.;
RT "Two new missense mutations (P134T and A244V) in the coagulation factor VII gene." ;

Query Match 81.2%; Score 161.5; DB 1; Length 466;
Best Local Similarity 75.6%; Pred. No. 8.5e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRPGSLXRXKXXQCFSFXARXIFPKDAERTKLFWISY 45
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Db 61 ANA-FLEELRPGSLERECKEQCSFEAREIFKDAERTKLFWISY 104

RESULT 2
Q96PQ8 PRELIMINARY; PRT; 679 AA.
AC Q96PQ8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF272774; AAKS8686.2; -;
DR HSSP; P08709; 1KLI.
DR GO; GO:0005576; C:cytoplasmic ion binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; ASX hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig_cI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001254; Peptide S1.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGcI; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 679 AA; 75552 MW; OB0023AE70A067AL CRC64.


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DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR001010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Calcium-binding; Direct protein sequencing;
KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;
KW Plasma; Repeat; Serine protease; Vitamin K; Zymogen.
FT CHAIN 1 152 Factor VII light chain.
FT CHAIN 153 407 Factor VII heavy chain.
FT DOMAIN 153 407 Gla.
FT DOMAIN 1 45 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 46 82 EGF-like 2.
FT DOMAIN 87 128 Serine protease.
FT DOMAIN 153 407 Cleavage (by factor Xa, factor XIIa,
FT SITE 152 153 factor IXa, or thrombin).
FT ACT_SITE 193 193 By similarity.
FT ACT_SITE 242 242 By similarity.
FT ACT_SITE 344 344 By similarity.
FT BINDING 338 338 Substrate (By similarity).
FT DISULFID 17 22 By similarity.
FT DISULFID 50 61 By similarity.
FT DISULFID 55 70 By similarity.
FT DISULFID 72 81 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 98 112 By similarity.
FT DISULFID 114 127 By similarity.
FT DISULFID 135 262 By similarity.
FT DISULFID 159 164 By similarity.
FT DISULFID 178 194 By similarity.
FT DISULFID 310 329 By similarity.
FT DISULFID 340 368 By similarity.
FT MOD_RES 6 6 4-carboxyglutamate.
FT MOD_RES 7 7 4-carboxyglutamate.
FT MOD_RES 14 14 4-carboxyglutamate.
FT MOD_RES 16 16 4-carboxyglutamate.
FT MOD_RES 19 19 4-carboxyglutamate.
FT MOD_RES 20 20 4-carboxyglutamate.
FT MOD_RES 25 25 4-carboxyglutamate.
FT MOD_RES 26 26 4-carboxyglutamate.
FT MOD_RES 29 29 4-carboxyglutamate.
FT MOD_RES 35 35 4-carboxyglutamate.
FT CARBOHYD 52 52 O-linked (Glc...).
FT CARBOHYD 145 145 N-linked (GlcNAc...).
FT CARBOHYD 203 203 N-linked (GlcNAc...).
SQ SEQUENCE 407 AA; 44431 MW; 703E1FE06367F7E10 CRC64;

Query Match 56.8%; Score 113; DB 1; Length 407;
Best Local Similarity 51.2%; Pred. No. 3.1e-11;
Matches 21; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 5 FLXXLRPGSLKRXCKXXQCSPXXARXIFKDXARTKLFWSY 45
DB 4 FLEELLPGSLERECREELCSFEEAHEIFRNEERTQFWVSY 44
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RESULT 6
Q8JHC9 PRELIMINARY; PRT; 443 AA.
AC Q8JHC9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Coagulation factor VIIi.
GN Name=f7i;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Hanumanthaiah R.; Day K.; Jagadeeswaran P.;
RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
RT Evolution of coagulation factor genes and identification of zebrafish
RT factor VIIi.";
RL Blood Cells Mol. Dis. 0:0-0(2002).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF519546; AAM88342.1; -.
DR EMBL; AF515269; AAN71000.1; -.
DR HSPSP; P00740; 1CFH.
DR ZFIN; ZDB-GENE-021206-10; f7i.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;

Query Match 54.8%; Score 109; DB 2; Length 443;
Best Local Similarity 44.4%; Pred. No. 1.8e-10;
Matches 20; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAYFLXLRPGSLKRXCKXXQCSPXXARXIFKDXARTKLFWSY 45
DB 38 ANSGFLEEMKAGNLERECVEECIDYEAREVEFDDRTKQFWLSY 82

RESULT 7
PRTC_PIG STANDARD; PRT; 459 AA.
AC Q9GLP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

25-OCT-2004 (Rel. 45, Last annotation update)
 Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 (Autoproteolytic cleavage of protein C) (Blood coagulation factor XIV).
 Name=PROG;
 Sub scrofa (Pig).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21121490; PubMed=11229814;
 RA Gram D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J., Kim H.K.W.;
 RA "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains.";
 RT domains.";
 RT Cell. Mol. Life Sci. 58:148-159(2001).
 RL -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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 EMBL; AF191307; AAG28380.1; -;
 HSSP; P04070; 1AUT.
 MEROPS; S01.218; -;
 InterPro; IPR000152; Asx_hydroxyl_S.
 InterPro; IPR000742; EGF 2.
 InterPro; IPR001881; EGF Ca.
 InterPro; IPR006209; EGF like.
 InterPro; IPR002383; GLA blood.
 InterPro; IPR006210; IEGF.
 InterPro; IPR009003; Pept_Ser_Cys.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR000294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; Gla; 1.
 Pfam; PF00899; Trypsin; 1.
 PRINTS; PR00722; GLYMOTRYPIN.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00181; EGF; 2.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; Tryp_SPc; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00998; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation; Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 41 By similarity.
 FT CHAIN 42 459 Vitamin K-dependent protein C.
 FT CHAIN 42 196 Vitamin K-dependent protein C light chain (By similarity).
 FT CHAIN 199 459 Vitamin K-dependent protein C heavy chain (By similarity).
 FT PEPTIDE 199 213 Activation peptide (By similarity).
 FT SITE 213 214 Cleavage (by thrombin) (By similarity). Gla.
 FT DOMAIN 42 87 EGF-like 1.
 FT DOMAIN 96 131 EGF-like 2.
 FT DOMAIN 135 175 Serine protease.
 FT DOMAIN 214 459 4-carboxyglutamate (By similarity).
 FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
 FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE 255 255 Charge relay system.
 FT ACT_SITE 301 301 Charge relay system.
 FT ACT_SITE 400 400 Charge relay system.
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 110 By similarity.
 FT DISULFID 100 105 By similarity.
 FT DISULFID 104 119 By similarity.
 FT DISULFID 121 130 By similarity.
 FT DISULFID 139 150 By similarity.
 FT DISULFID 146 159 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 182 321 Interchain (By similarity).
 FT DISULFID 240 256 By similarity.
 FT DISULFID 371 385 By similarity.
 FT DISULFID 396 424 By similarity.
 FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 52.0%; Score 103.5; DB 1; Length 459;
 Best Local Similarity 48.9%; Pred. No. 1.7e-09;
 Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;
 Qy 1 ANAYFLXLRPGSLRXKXQCSFXRXARXIFKDXRKLFWISY 45
 Db 42 ANS-FLBELPSSLERECKETCDFFBEAREIFQNTENTMAFWSKY 85
 RESULT 8
 PRTC MOUSE
 ID_PRTC_MOUSE STANDARD; PRT; 460 AA.
 AC P33587; O35498; Q91WN8; Q99PC6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic cleavage of protein C) (Blood coagulation factor XIV).

GN Name=Proc;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=92316897; PubMed=1618739;
 RA Tada N., Sato M., Tsuchimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Roben E.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 RT anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Korf I.;
 RT "Complete sequence of UC72A01.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 274-433 FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=94318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
 RT "A comparative study of partial primary structures of the catalytic
 RT region of mammalian protein C.";
 RL Br. J. Haematol. 86:590-600(1994).
 CC CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIIIa
 CC in the presence of calcium ions and phospholipids.
 CC CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIIa.
 CC CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetradecapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC CC -1- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.

CC CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the thrombin-
 CC thrombomodulin complex.
 CC CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (GLA)
 CC domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D10445; BAA01235.1; -;
 CC EMBL; AF034569; AAC33795.1; -;
 CC EMBL; AF318182; AAK07918.1; -;
 CC EMBL; BC013896; AAH13896.1; -;
 CC EMBL; D43755; BAA07812.1; -;
 CC PIR; JX0210; JX0210.
 CC HSSP; P04070; LAUT.
 CC MEROPS; S01.218; -;
 CC MGD; MGI:97771; Proc.
 CC InterPro; IPR000152; Asx_hydroxyl_1.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR002383; GLA_blood.
 CC InterPro; IPR009003; Pept_Ser_Cys.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_GLA.
 CC InterPro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; Gla; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00179; EGF_CA; 1.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS00026; EGF_3; 1.
 CC PROSITE; PS01187; EGF_CA; 1.
 CC PROSITE; PS00011; GLA_1; 1.
 CC PROSITE; PS50998; GLA_2; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Calcium-binding; EGF-like domain;
 CC Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 CC Repeat; Serine protease; Signal; Vitamin K.
 CC SIGNAL 1 33 By similarity.
 CC PROPEP 3 41 By similarity.
 CC CHAIN 42 460 Vitamin K-dependent protein C.
 CC CHAIN 42 196 Vitamin K-dependent protein C light chain
 CC (By similarity).
 CC CHAIN 199 460 Vitamin K-dependent protein C heavy chain
 CC (By similarity).
 CC PEPTIDE 199 212 Activation peptide (By similarity).
 CC SITE 212 213 Cleavage (by thrombin) (By similarity).
 CC DOMAIN 42 87 Gla.
 CC DOMAIN 96 131 EGF-like 1.
 CC DOMAIN 135 175 EGF-like 2.
 CC DOMAIN 213 460 Serine protease.
 CC MOD_RES 47 47 4-carboxyglutamate (By similarity).
 CC MOD_RES 48 48 4-carboxyglutamate (By similarity).
 CC MOD_RES 55 55 4-carboxyglutamate (By similarity).
 CC MOD_RES 57 57 4-carboxyglutamate (By similarity).

RESULT	9
ID	Q8TAS3
DB	PRELIMINARY; PRT; 179 AA.
AC	Q8TAS3;
DT	01-JUN-2002 (TEMBLrel. 21, Created)
DD	01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT	01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE	PRRG2 protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Placenta;
RE	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Muszy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA	Jones S.-J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Placenta;

Strausberg R.;

Submitted (MAR-2002) to the EMBL/GenBank/DBAJ databases.

EMBL; BC026032; AAH26032.1; -.

HSP; P00740; 1CPH.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

InterPro; IPR002383; GLA blood.

InterPro; IPR000294; VitC_dep_GLA.

Fam; PF00594; GLA; 1.

PRINTS; PR00001; GLABLOOD.

SMART; SM00069; GLA; 1.

PROSITE; PS00011; GLA 1; 1.

SEQUENCE 179 AA; 19819 MW; 8A948A3D4C1E5378 CRC64;

Query Match 48.2%; Score 96; DB 2; Length 179;

Best Local Similarity 44.4%; Pred. NO. 1.4e-08;

Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps

QY 1 ANAYFLXLRPGSLRXCKXCQCSPFXRXRXFKDAXRTKLEWISY 45

27 ANHWDELTPGNLRCELCERCSWEAREYFEDNTLTERFWEYSY 71

DB

RESULT 10

TMG2 MOUSE

ID TMG2_MOUSE STANDARD; PRT; 198 AA.

AC Q9R182; Q95012;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Transmembrane gamma-carboxylglutamic acid protein 2 precursor (Proline-rich Glu protein 2) (Proline-rich gamma-carboxylglutamic acid protein 2) (Nedd4 WW domain-binding protein 1).

DE 2) (Nedd4 WW domain-binding protein 1).

OS Mus musculus (Mouse).

GN Names=Prrg2; Synonyms=N4WBPI;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

TISSUE=Liver;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.W., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley A.C., Grimwood J.W., Green E.D., Dickson M.C., Rodriguez A.C., Touchman J.J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE OF 114-198 FROM N.A.

MEDLINE=20498735; PubMed=11042109; DOI=10.1042/0264-6021:3510557;

Jolliffe C.N., Harvey K.F., Haines B.P., Parasivam G., Kumar S.;

"Identification of multiple proteins expressed in murine embryos as binding partners for the WW domains of the ubiquitin-protein ligase Rbtd4."

Biochem. J. 351:557-565(2000).

-!- SUBUNIT: Binds NEDD4 (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-!- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-carboxylase (By similarity).

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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EMBL: BC025098; AAH25098.1; -.

EMBL: AF220205; AAG44244.1; -.

HSSP: P00740; ICFH.

MGI: 1925956; Prpg2.

GO: GO:0005515; F:protein binding; IPI.

InterPro: IPR002383; GLA_blood.

InterPro: IPR000294; VitK_dep_GLA.

Pfam: PF00594; Gla; 1.

PRINTS: PR00001; GLABLOOD.

SMART: SM00069; GLA; 1.

PROSITE: PS00011; GLA_1; 1.

PROSITE: PS00998; GLA_2; 1.

Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.

SIGNAL 1 20

FT PROPEP 21 51 By similarity.

FT CHAIN 52 198 Transmembrane gamma-carboxyglutamic acid

FT protein 2.

FT DOMAIN 52 111 Extracellular (Potential).

FT TRANSMEM 112 134 Potential.

FT DOMAIN 135 198 Cytoplasmic (Potential).

FT DOMAIN 52 97 Gla.

SQ SEQUENCE 198 AA; 1C6482C8445450FC CRC64;

Query Match 48.2%; Score 96; DB 1; Length 198;

Best Local Similarity 44.4%; Pred. No. 1.6e-08;

Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAYFLXLRPGSLXRXCKXQCQCFXKXIFKDXRTKLFWSY 45

Db 52 ANHWDELLTPGNLERCERCSWEAREYFEDNTLTERFWESY 96

RESULT 11

TW2 HUMAN STANDARD; PRT; 202 AA.

AC O14669;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Transmembrane gamma-carboxyglutamic acid protein 2 precursor (Proline-rich Gla protein 2)

DE rich Gla protein 2 (Proline-rich gamma-carboxyglutamic acid protein 2).

GN Name=PRPG2; Synonyms=PRGP2, TWG2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=97404347; PubMed=9256434; DOI=10.1073/pnas.94.17.9058;

RA Kulman J.D., Harris J.B., Haldeman B.A., Davie E.W.;

RT "Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins";

RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062 (1997).

CC -!- SUBUNIT: Binds NEDD4 (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in the thyroid.

-!- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-carboxylase.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

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EMBL: AF009243; AAB67071.1; -.

HSSP: P00740; ICFH.

Genew; HGNC:9470; PRRG2.

MIM: 604429; -.

GO: GO:0005887; C:integral to plasma membrane; TAS.

InterPro: IPR002383; GLA_blood.

InterPro: IPR011047; Quin_alc_DH_like.

InterPro: IPR000294; VitK_dep_GLA.

Pfam: PF00594; Gla; 1.

PRINTS: PR00001; GLABLOOD.

SMART: SM00069; GLA; 1.

PROSITE: PS00011; GLA_1; 1.

PROSITE: PS00998; GLA_2; 1.

Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.

SIGNAL 1 23

FT PROPEP 24 49

FT CHAIN 50 202 Transmembrane gamma-carboxyglutamic acid

FT protein 2.

FT DOMAIN 50 109 Extracellular (Potential).

FT TRANSMEM 110 132 Potential.

FT DOMAIN 133 202 Cytoplasmic (Potential).

FT DOMAIN 50 96 Gla.

FT DOMAIN 161 173 Poly-Pro.

FT DOMAIN 191 194 Poly-Pro.

SQ SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;

Query Match 48.2%; Score 96; DB 1; Length 202;

Best Local Similarity 44.4%; Pred. No. 1.6e-08;

Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANAYFLXLRPGSLXRXCKXQCQCFXKXIFKDXRTKLFWSY 45

Db 50 ANHWDELLTPGNLERCERCSWEAREYFEDNTLTERFWESY 94

RESULT 12

Q6DIH4 PRELIMINARY; PRT; 216 AA.

AC Q6DIH4;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Prpg4-prov protein.

GN Name=prpg4-prov;

OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8364;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA	Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RL	Klein S., Gerhard D.S.;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
DR	ENBL: BC075566; AAH75566.1; "
DR	GO: GO:0005576; C:extracellular; IEA.
DR	GO: GO:0005509; F:calcium ion binding; IEA.
DR	InterPro: IPR002383; GLA blood.
DR	InterPro: IPR002294; VitK_dep_GLA.
DR	Pfam: PF005594; Gla: 1.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM00069; GLA; 1.
DR	PROSITE; PS00011; GLA 1; 1.
DR	SEQUENCE 216 AA; 23721 MW; 790D18D0A2229087A CRC64;

Query Match	47.7%	Score 95;	DB 2;	Length 216;
Best Local Similarity	36.4%	Pred. No. 2.6e-08;		
Matches 20:	Conservative	8;	Mismatches 17;	Indels 10;
				Gaps 1;

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Qy 1 ANAYFLXXL-----RPGSLYXCKXXQCSFXFXAPXIFKDXARTKLFWISY 45
    |||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:|
Dp 50 ANAFFVRLLYNSWDFELVTPGNLRECYEEVCNYESARECFDOKTKTEWTKY 104

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RESULT 13
Q804X1
ID Q804X1 PRELIMINARY; PRT; 442 AA.
AC Q804X1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Coagulation factor VIIb (EC 3.4.21.21).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
RA Tuddenham E.G.D., McVey J.H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AF465274; A033369.1; -.
DR HSSP; P00740; 1CFH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:calmodulin activity; IEA.
DR GO; GO:0003802; P:coagulation factor VIIa activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA blood.

```

DR	InterPro	IPR006210	IEGF	
DR	InterPro	IPR001254	Peptidase_S1	
DR	InterPro	IPR001314	Peptidase_S1A	
DR	InterPro	IPR009003	Pept_Ser_Cys	
DR	InterPro	IPR000294	VitK_dep_GLA	
DR	Pfam	PF00008	EGF_2	
DR	Pfam	PF00594	Gla_1	
DR	Pfam	PF00089	Trypsin_1	
DR	PRINTS	PRO0722	CHYMOTRYPSIN	
DR	PRINTS	PRO0001	GLABLOOD	
DR	SMART	SM00181	EGF_2	
DR	SMART	SM00069	Gla_1	
DR	SMART	SM00020	Tryp_Spc_1	
DR	PROSITE	PS00022	EGF_1	UNKNOWN_1
DR	PROSITE	PS01186	EGF_2	
DR	PROSITE	PS00026	EGF_3	
DR	PROSITE	PS00011	Gla_1	
DR	PROSITE	PS00240	TRYPSIN_DOM	
DR	PROSITE	PS00134	TRYPSIN_HIS	UNKNOWN_1
KW	EGF-like domain	Hydrolase	Protease	Serine protease.
SQ	SEQUENCE	442 AA	48787 MW	810A561A127F0CF7 CRC64;

Query Match	47.2%	Score 94	DB 2	Length 442
Best Local Similarity	37.8%	Pred.No. 8.2e-08		
Matches 17	Conservative 11	Mismatches 17	Indels	

Qy	1	ANAYFLXLRPSGLRXKCKXQGSFXKXARXIFKDXARTKLFWSY	45
Db	38	ANSGLFEEMQQGNLKECTIEICNYEAREVFEDDAQTRKFWET	82

RESULT 14			
QD04X7	PRELIMINARY	PRT	425 AA
AC	Q804X7		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Coagulation factor VII (EC 3.4.21.21)		
OS	Gallus gallus (Chicken)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Aves; Neognathae; Galliformes; Phasianidae; P		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; P		
OC	Gallus		
CC	NCBI_TaxID=9031;		
CC	SEQUENCE FROM N.A.		
RP	Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,		
RA	Tuddenham E.G.D., McVey J.H.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: Belongs to peptidase family S1.		
CC	-!- SIMILARITY: Contains 1 EGF-like domain.		
DR	EMBL; AF465268; AAO33363.1; --		
DR	HSPR; P08709; 1KLJ;		
DR	MEROFS; S01.215; --		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0003802; F:coagulation factor VIIa activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR000152; Asx hydroxyl_S.		
DR	InterPro; IPR000742; EGF_2		
DR	InterPro; IPR001881; EGF_Ca		
DR	InterPro; IPR001438; EGF_I1		
DR	InterPro; IPR006209; EGF_like		
DR	InterPro; IPR002383; GLA_blood		
DR	InterPro; IPR006210; IEGF		
DR	InterPro; IPR001254; Peptidase_S1		
DR	InterPro; IPR001314; Peptidase_S1A		
DR	InterPro; IPR009003; Pept_Ser_Cys		
DR	InterPro; IPR000294; VitK_dep_GLA		
DR	Pfam; PF00008; EGF_1		

DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGF-BLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; Gla; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 425 AA; 47626 MW; 36A69BF0DB8C6DAC CRC64;
 Query Match 47.0%; Score 93.5; DB 2; Length 425;
 Best Local Similarity 44.4%; Pred. No. 9.6e-08;
 Matches 20; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
 Qy 1 ANAYFLXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWSY 45
 Db 41 ANSFF-BEIKLGLPERECIEBKCSFEAREIYRDERTKSFWHY 84
 RESULT 15
 FA7_RAT STANDARD; PRT; 446 AA.
 AC Q8K3U6;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 DE Name=P7;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=Sprague-Dawley;
 RA Murphy K., Ramaker M.;
 RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Initiates the extrinsic pathway of blood coagulation.
 CC Serine protease that circulates in the blood in a zymogen form.
 CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa,
 CC factor IXa, or thrombin by minor proteolysis. In the presence of
 CC tissue factor and calcium ions, factor VIIa then converts factor X
 CC to factor Xa by limited proteolysis. Factor VIIa will also convert
 CC factor IX to factor IXa in the presence of tissue factor and
 CC calcium (By similarity).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
 CC a disulfide bond (By similarity).
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
 CC glutamate residues allows the modified protein to bind calcium (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR HMBL; AF532184; AAM95967.1; -.
 DR HSP; P08709; 1KLJ.
 DR RGD; 628678; F7.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF-II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGF-BLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; Gla; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00098; GLA_2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 41 Potential.
 FT CHAIN 42 193 Factor VII light chain (By similarity).
 FT CHAIN 194 446 Factor VII heavy chain (By similarity).
 FT DOMAIN 42 86 Gla.
 FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
 FT DOMAIN 128 169 EGF-like 2.
 FT DOMAIN 194 446 Serine protease.
 FT SITE 193 194 Cleavage (by factor Xa, factor XIIa,
 FT factor IXa, or thrombin) (By similarity).
 FT ACT_SITE 234 234 By similarity.
 FT ACT_SITE 283 283 By similarity.
 FT ACT_SITE 385 385 By similarity.
 FT BINDING 379 379 Substrate (By similarity).
 FT DISULFID 58 63 By similarity.
 FT DISULFID 91 102 By similarity.
 FT DISULFID 96 111 By similarity.
 FT DISULFID 113 122 By similarity.
 FT DISULFID 132 143 By similarity.
 FT DISULFID 139 153 By similarity.
 FT DISULFID 155 168 By similarity.
 FT DISULFID 176 303 By similarity.
 FT DISULFID 200 205 By similarity.
 FT DISULFID 219 235 By similarity.
 FT DISULFID 351 370 By similarity.
 FT DISULFID 381 409 By similarity.
 FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES 60 60 4-carboxyglutamate (By similarity).

FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 76 76 4-carboxyglutamate (By similarity).
FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 446 AA; 50399 MW; 292985EBF119C0AA CRC64;

Query Match 47.0%; Score 93.5; DB 1; Length 446;
Best Local Similarity 48.9%; Pred. No. 1e-07;
Matches 22; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

Oy 1 ANAYFLXXLRPGSLRXKXXQCSPFXAXRIFKDXRTKLFWISY 45
||:| | | | | :||| | | | | | | | | | | | | | |
Db 42 ANS-LLEELWSSSLERECNEERCSPFEAREIFKSPERTKQFWTIY 85

Search completed: August 22, 2005, 18:42:25
Job time : 85 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	161.5	81.2	44	3	US-08-955-636-3	Sequence 3, Appli
2	161.5	81.2	44	4	US-09-302-232-3	Sequence 3, Appli
3	161.5	81.2	44	4	US-09-497-591-3	Sequence 3, Appli
4	161.5	81.2	44	4	US-08-803-810-3	Sequence 3, Appli
5	161.5	81.2	406	1	US-08-293-778-24	Sequence 24, Appli
6	161.5	81.2	406	1	US-08-295-411-5	Sequence 5, Appli
7	161.5	81.2	406	2	US-08-955-471-5	Sequence 5, Appli
8	161.5	81.2	406	4	US-09-782-587B-1	Sequence 1, Appli
9	161.5	81.2	406	4	US-09-782-587B-3	Sequence 3, Appli
10	161.5	81.2	406	5	PCR-US92-10242-5	Sequence 5, Appli
11	161.5	81.2	444	1	US-08-475-845-2	Sequence 2, Appli
12	161.5	81.2	444	2	US-08-327-690-2	Sequence 2, Appli
13	161.5	81.2	444	2	US-08-660-289-2	Sequence 2, Appli
14	161.5	81.2	444	2	US-08-537-807-2	Sequence 2, Appli
15	161.5	81.2	444	2	US-08-871-003-2	Sequence 2, Appli
16	161.5	81.2	444	3	US-08-464-233-2	Sequence 2, Appli
17	161.5	81.2	444	3	US-09-189-607-2	Sequence 2, Appli
18	161.5	81.2	444	3	US-09-378-907-2	Sequence 2, Appli
19	161.5	81.2	444	5	PCR-US94-05779-2	Sequence 2, Appli
20	161.5	81.2	461	4	US-09-949-016-8839	Sequence 8839, Ap
21	161.5	81.2	466	1	US-07-882-202A-4	Sequence 4, Appli
22	161.5	81.2	466	1	US-08-021-615A-4	Sequence 4, Appli
23	161.5	81.2	466	1	US-08-321-777-4	Sequence 4, Appli
24	161.5	81.2	466	3	US-09-009-217-14	Sequence 14, Appli
25	161.5	81.2	466	3	US-09-009-656-14	Sequence 14, Appli
26	161.5	81.2	466	5	PCR-US93-04493-4	Sequence 4, Appli
27	161.5	81.2	483	4	US-09-949-016-9523	Sequence 9523, Ap

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-302-239-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 44

RESULT 3
US-09-497-591-3
; Sequence 3, Application US/09497591
; Patent No. 6747003
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531-016001
; CURRENT APPLICATION NUMBER: US/09/497,591
; CURRENT FILING DATE: 2000-02-03
; EARLIER APPLICATION NUMBER: 09/302,239
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: 08/955,636
; EARLIER FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-497-591-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 44

RESULT 4
US-09-803-810-3
; Sequence 3, Application US/09803810
; Patent No. 6762286
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-09-803-810-3

Query Match 81.2%; Score 161.5; DB 4; Length 44;
Best Local Similarity 97.8%; Pred. No. 1.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 44

RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
; FILING DATE: 24-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,248
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3129.224-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-293-778-24

Query Match 81.2%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXLRPGSLXRCXKXQCXFFXXARXIFKDXARTKLFWISY 45
Db 1 ANA-FLYLRPGSLRYCKYQCXFFYYIFKDAYRTKLFWISY 44

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RESULT 6
US-08-295-411-5
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; Query Match 81.2%; Score 161.5; DB 1; Length 406;
; Best Local Similarity 75.6%; Pred. No. 1e-18;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXLRPGSLRXCKXQCSCFXRXARXIFKDXRKLFWISY 45
DB 1 ANA-FLBELRPGSLRECKEBCQCSFEAREIFKDAERTKLFWISY 44

RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
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; APPLICANT: Griffin, John H.
; APPLICANT: Mesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
;
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
;
; US-08-955-471-5
;
; Query Match 81.2%; Score 161.5; DB 2; Length 406;
; Best Local Similarity 75.6%; Pred. No. 1e-18;
; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 ANAYFLXLRPGSLRXCKXQCSCFXRXARXIFKDXRKLFWISY 45
DB 1 ANA-FLBELRPGSLRECKEBCQCSFEAREIFKDAERTKLFWISY 44

RESULT 8
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
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;; PRIOR APPLICATION NUMBER: PA 2000 00218
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: 60/184,036
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/241,916
;; PRIOR FILING DATE: 2000-10-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 406
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MOD RES
;; LOCATION: (6)..(7)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (14)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (16)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (19)..(20)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (25)..(26)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (29)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
;; NAME/KEY: MOD RES
;; LOCATION: (35)
;; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match 81.2%; Score 161.5; DB 4; Length 406;
Best Local Similarity 97.6%; Pred. No. 1e-18;
Matches 44; Conservative 0; Mismatches 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 9
US-09-782-587B-3
;; Sequence 3, Application US/09782587B
;; Patent No. 6806063
;; GENERAL INFORMATION:
;; APPLICANT: PEDERSEN, ANDERS H.
;; APPLICANT: ANDERSON, KIM V.
;; APPLICANT: BORNAES, CLAUS
;; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
;; FILE REFERENCE: 31-001100US
;; CURRENT APPLICATION NUMBER: US/09/782,587B
;; CURRENT FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: PA 2000 00218
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: 60/184,036
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: 60/241,916
;; PRIOR FILING DATE: 2000-10-18
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 406
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match 81.2%; Score 161.5; DB 4; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18;

Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLEELRPGSLERECKEEQCSFEAREIFKDXRTKLFWISY 44
RESULT 10
PCT-US92-10242-5
;; Sequence 5, Application PC/TUS9210242
;; GENERAL INFORMATION:
;; APPLICANT: Griffin, John H.
;; APPLICANT: Meesters, Rolf
;; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
;; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
;; TITLE OF INVENTION: for Inhibiting Coagulation
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Office of Patent Counsel, The Scripps
;; ADDRESSEE: Research Institute
;; STREET: 10666 North Torrey Pines Road, TPC 8
;; CITY: La Jolla
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/10242
;; FILING DATE: 19921118
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/793,989
;; FILING DATE: 18-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitting, Thomas
;; REGISTRATION NUMBER: 34,163
;; REFERENCE/DOCKET NUMBER: SCRO472P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-554-2937
;; TELEFAX: 619-554-6312
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 406 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 1..152
;; OTHER INFORMATION: /note= "Factor VII Light Chain"
;; FEATURE:
;; NAME/KEY: Region
;; LOCATION: 153..406
;; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 81.2%; Score 161.5; DB 5; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCKXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLEELRPGSLERECKEEQCSFEAREIFKDXRTKLFWISY 44

RESULT 11
US-08-475-845-2


```

1 ; NUMBER OF SEQUENCES: 4
2 ; CORRESPONDENCE ADDRESS:
3 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
4 ; STREET: One Market Plaza, Steuart Street Tower
5 ; CITY: San Francisco
6 ; STATE: CA
7 ; COUNTRY: U.S.A.
8 ; ZIP: 94105-1492
9 ; COMPUTER READABLE FORM:
10 ; MEDIUM TYPE: Floppy disk
11 ; COMPUTER: IBM PC compatible
12 ; OPERATING SYSTEM: PC-DOS/MS-DOS
13 ; SOFTWARE: PatentIn Release #1.24
14 ;
15 ; CURRENT APPLICATION DATA:
16 ; APPLICATION NUMBER: US/08/327,690
17 ; FILING DATE: 24-OCT-1994
18 ; CLASSIFICATION: 435
19 ;
20 ; PRIOR APPLICATION DATA:
21 ; APPLICATION NUMBER: 08/065,725
22 ; FILING DATE: 21-MAY-1993
23 ; CLASSIFICATION: 435
24 ;
25 ; PRIOR APPLICATION DATA:
26 ; APPLICATION NUMBER: 07/662,920
27 ; FILING DATE: 28-FEB-1991
28 ; CLASSIFICATION: 435
29 ;
30 ; ATTORNEY/AGENT INFORMATION:
31 ; NAME: Parmelee, Steven W.
32 ; REGISTRATION NUMBER: 31,990
33 ; REFERENCE/DOCKET NUMBER: 13952-8-3
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: 206-467-9600
36 ; TELEFAX: 415-543-5043
37 ; INFORMATION FOR SEQ ID NO: 2:
38 ; SEQUENCE CHARACTERISTICS:
39 ; LENGTH: 444 amino acids
40 ; TYPE: amino acid
41 ; TOPOLOGY: linear
42 ; MOLECULE TYPE: protein
43 ;
44 ; US-08-327-690-2
45 ;
46 ; Query Match 81.2%; Score 161.5; DB 2; Length 444;
47 ; Best Local Similarity 75.6%; Pred. No. 1.1e-18;
48 ; Matches 34; Conservative 0; Mismatches 10; Indels 1
49 ;
50 ; QY 1 ANAYFLXXLRPGSLXRCXKXQCSFFXAXRIFKDXATKLFWSY 45
51 ; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
52 ; 39 ANA-FLSELRPGSLERCKEKCQCSFEAREIFKDAERTKLFWSY 82
53 ; ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
54 ;
55 ; RESULT 13
56 ; US-08-660-289-2
57 ; Sequence 2, Application US/08660289
58 ; Patent No. 5833982
59 ;
60 ; GENERAL INFORMATION:
61 ; APPLICANT: Berkner, Kathleen L.
62 ; APPLICANT: Petersen, Lars C.
63 ; APPLICANT: Hart, Charles E.
64 ; APPLICANT: Hedner, Ulla
65 ; APPLICANT: Bregengaard, Claus
66 ; TITLE OF INVENTION: Modified Factor VII
67 ;
68 ; NUMBER OF SEQUENCES: 4
69 ; CORRESPONDENCE ADDRESS:
70 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
71 ; STREET: One Market Plaza, Steuart Street Tower
72 ; CITY: San Francisco
73 ; STATE: CA
74 ; COUNTRY: U.S.A.
75 ; ZIP: 94105-1492
76 ; COMPUTER READABLE FORM:
77 ; MEDIUM TYPE: Floppy disk
78 ; COMPUTER: IBM PC compatible
79 ; OPERATING SYSTEM: PC-DOS/MS-DOS
80 ; SOFTWARE: PatentIn Release #1.24

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,289
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,845
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/327,690
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-289-2

Query Match 81.2%; Score 161.5; DB 2; Length 444;
Best Local Similarity 75.6%; Pred. No. 1.1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCQCFXXARXIFKDXRTKLFWISY 45
Db 39 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-537-807-2
; Sequence 2, Application US/08537807
; Patent No. 5861374
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05779
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 08/065,725
; FILING DATE: 21-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,920
; FILING DATE: 28-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
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;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match 81.2%; Score 161.5; DB 2; Length 444;
Best Local Similarity 75.6%; Pred. No. 1.1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCQCFXXARXIFKDXRTKLFWISY 45
Db 39 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-871-003-2
; Sequence 2, Application US/08871003
; Patent No. 5997864
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hedner, Ulla
; APPLICANT: Rasmussen, Mirella E.
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,003
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 90-07C7
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-003-2

Query Match 81.2%; Score 161.5; DB 2; Length 444;
Best Local Similarity 75.6%; Pred. No. 1.1e-18;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKCKXXQCQCFXXARXIFKDXRTKLFWISY 45
Db 39 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: August 22, 2005, 18:47:55
Job time : 31 secs
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RESULT 2
US-10-298-330-3

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; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIITA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxylglutamic acid or glutamic acid
; US-09-782-587B-1
Best Match      81.2%; Score 161.5; DB 10; Length 406;
Query Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY    1 ANAYFLXLRPGSLXRXCXXQCSPFXRXRXPFDAXRXTKLFWISY 45
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Db     1 ANA-FLXLRLPGLXRRCXXQCSPFXRXRXPFDAXRXTKLFWISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIITA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match      81.2%; Score 161.5; DB 10; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 6
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286.200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 44

RESULT 7
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A10 No. US20030100075Aldisk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

US-10-255-032-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 44

RESULT 8
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Human Coagulation Factor VII
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1

Query Match      81.2%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXCKXXCQSFXXARXIFKDXRXTKLFWISY 44

RESULT 9
US-10-386-898-7
; Sequence 7, Application US/10386898
; Publication No. US20030229018A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030229018A10 No. US20030229018Aldisk Pharmaceuticals, Inc.
; APPLICANT: Kjalke, Marianne
; APPLICANT: Jakobsen, Palle
; APPLICANT: Stennicke, Henning Ralf
; TITLE OF INVENTION: DIMERIC TF ANTAGONIST
; FILE REFERENCE: 6445.200-US
; CURRENT APPLICATION NUMBER: US/10/386,898
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US 60/365,935
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
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; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-386-898-7

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 10

US-10-383-898-1
; Sequence 1, Application US/10383898
; Publication No. US20040009914A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Curcuminoid-protein conjugates
; FILE REFERENCE: E056 1060.1
; CURRENT APPLICATION NUMBER: US/10/383,898
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(406)

US-10-383-898-1

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 11

US-10-617-500-1
; Sequence 1, Application US/10617500
; Publication No. US20040072753A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Stennicke, Henning R
; APPLICANT: Bjorn, Soren E
; APPLICANT: Petersen, Lars C
; TITLE OF INVENTION: TF Antagonist
; FILE REFERENCE: 6510.200-US
; CURRENT APPLICATION NUMBER: US/10/617,500
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,567
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(406)

; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)

US-10-617-500-1

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 12

US-10-263-205B-2
; Sequence 2, Application US/10263205B
; Publication No. US20040087498A1
; GENERAL INFORMATION:
; APPLICANT: BERKNER, Kathleen L.
; APPLICANT: PETERSEN, Lars
; APPLICANT: HART, Charles E.
; APPLICANT: HEDNER, Ulla
; APPLICANT: BREGENGAARD, Claus
; TITLE OF INVENTION: MODIFIED FACTOR VII
; FILE REFERENCE: 13952N-8-5-1
; CURRENT APPLICATION NUMBER: US/10/263,205B
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/464,029
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/327,690
; PRIOR FILING DATE: 1994-10-24
; PRIOR APPLICATION NUMBER: PCT/US94/05779
; PRIOR FILING DATE: 1994-05-23
; PRIOR APPLICATION NUMBER: 08/065,725
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: PCT/US92/01636
; PRIOR FILING DATE: 1991-02-28
; PRIOR APPLICATION NUMBER: 07/662,920
; PRIOR FILING DATE: 1991-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-263-205B-2

Query Match 81.2%; Score 161.5; DB 15; Length 406;
Best Local Similarity 75.6%; Pred. No. 4.1e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXKXXQCXXQCSFXXARXIFKDXRTKLFWISY 45
Db 1 ANA-FLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 44

RESULT 13

US-10-617-619-1
; Sequence 1, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT

; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(406)
 ; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-617-619-1

Query Match 81.2%; Score 161.5; DB 16; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRGSLRXKCKXQCSPFXAXRXPDKAXRTKLFWISY 45
 ||| |||||
 Db 1 ANA-FLXXLRGSLRXKCKXQCSPFXAXRXPDKAXRTKLFWISY 44
 ||| |||||

RESULT 14
 US-10-701-294-1
 ; Sequence 1, Application US/10701294
 ; Publication No. US20040143099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Petersen, Lars C
 ; APPLICANT: Back, Jakob M
 ; APPLICANT: Meyer, Christian
 ; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
 ; FILE REFERENCE: 6608.200-US
 ; CURRENT APPLICATION NUMBER: US/10/701,294
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: US 60/434,904
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
 ; PRIOR FILING DATE: 2002-11-06
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: human coagulation Factor VII
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(406)
 ; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-701-294-1

Query Match 81.2%; Score 161.5; DB 16; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ANAYFLXXLRGSLRXKCKXQCSPFXAXRXPDKAXRTKLFWISY 45
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 Db 1 ANA-FLXXLRGSLRXKCKXQCSPFXAXRXPDKAXRTKLFWISY 44
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RESULT 15
 US-10-669-537-1
 ; Sequence 1, Application US/10669537
 ; Publication No. US20040192602A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Persson, Egon
 ; APPLICANT: Olsen, Ole Hvilsted
 ; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
 ; FILE REFERENCE: 6544.200-US
 ; CURRENT APPLICATION NUMBER: US/10/669,537
 ; CURRENT FILING DATE: 2003-09-24
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
 ; PRIOR FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 60/417,927
 ; PRIOR FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 13

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